

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2005, 06:34:51 ; Search time 40 Seconds  
(without alignments)  
584.517 Million cell updates/sec

Title: US-10-662-431-2\_COPY\_39\_281  
Perfect score: 1287  
Sequence: 1 TNELKQMDKYKSGIACFL.....NEHLMDHSAFFGAFVLVG 243

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 125689

Minimum DB seq length: 0

Maximum DB seq length: 243

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134.5	10.5	204	1 S17289	tumor necrosis fac
2	131.5	10.2	234	1 A25451	tumor necrosis fac
3	130	10.1	232	1 S12606	tumor necrosis fac
4	129.5	10.1	235	2 I54490	tumor necrosis fac
5	127.5	9.9	204	1 S24641	lymphotoxin - bovi
6	126	9.8	234	1 JQ1344	tumor necrosis fac
7	123	9.6	233	1 QWHUN	tumor necrosis fac
8	122	9.5	205	1 QWHUX	lymphotoxin alpha
9	121	9.4	235	1 QWMSN	tumor necrosis fac
10	121	9.4	235	2 JU0029	tumor necrosis fac
11	120	9.3	233	1 S22052	tumor necrosis fac
12	117.5	9.1	234	1 JH0529	tumor necrosis fac
13	115.5	9.0	193	2 S06192	tumor necrosis fac
14	114	8.9	202	1 B27303	tumor necrosis fac
15	113.5	8.8	185	2 S52715	tumor necrosis fac
16	113	8.8	233	1 S24642	tumor necrosis fac
17	111.5	8.7	202	1 JN0869	tumor necrosis fac
18	107	8.3	197	1 JH0309	tumor necrosis fac
19	98.5	7.7	233	2 S11688	tumor necrosis fac
20	80.5	6.3	203	2 C98803	hypothetical prote
21	78	6.1	202	2 A82076	conserved hypotbet
22	77	6.0	223	2 H71485	hypothetical prote
23	76.5	5.9	195	2 S77753	peptide transport
24	75.5	5.9	142	2 B87569	dnak suppressor pr
25	74	5.7	201	2 E82910	hypothetical prote
26	73	5.7	223	2 B64396	hypothetical prote
27	73	5.7	227	2 B70438	hypothetical prote
28	72.5	5.6	112	2 A70347	conserved hypotbet
29	72.5	5.6	123	2 T26862	hypothetical prote

30	72.5	5.6	156	2 H71623	probable secreted
31	72.5	5.6	218	2 A99014	hypothetical prote
32	72.5	5.6	243	2 A99387	SAW-dependent math
33	71.5	5.6	195	1 I40422	conserved hypotbet
34	71.5	5.6	227	2 H64336	formate dehydrogen
35	71	5.5	234	2 T21543	hypothetical prote
36	70.5	5.5	189	2 D45188	chitin synthase (E
37	70.5	5.5	222	2 T37839	hypothetical prote
38	70.5	5.5	226	2 C81749	conserved hypotbet
39	70	5.4	209	2 D90593	lipoprotein (impor
40	69.5	5.4	144	2 H81292	hypothetical prote
41	69.5	5.4	199	2 J80351	OX40 ligand protei
42	69.5	5.4	201	2 S53800	chitin synthase (E
43	69.5	5.4	202	2 B90180	ABC transporter, A
44	69.5	5.4	222	2 A81896	hypothetical prote
45	69	5.4	139	2 T28300	ORF MSV139 hypothe

#### ALIGNMENTS

##### RESULT 1

S17289

tumor necrosis factor beta precursor - pig

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C/Accession: S17289

R/Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.

Gene 102, 171-178, 1991

A/Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal

A/Reference number: S17289; MUID:91340150; PMID:1874444

A/Accession: S17289

A/Molecule type: DNA

A/Residues: 1-204 <KUH>

A/Cross-references: UNIPROT:P26445; EMBL:X54859; NID:g2132; PIDN:CAA38638.1; PID:g2133

C/Genetics:

A/Introns: 32/3; 68/1

C/Superfamily: tumor necrosis factor

C/Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

F/1-33/Domain: signal sequence #status predicted <SIG>

F/34-204/Product: tumor necrosis factor beta #status predicted <MAT>

Query Match 10.5%; Score 134.5; DB 1; Length 204;  
Best Local Similarity 24.7%; Pred. No. 0.00039;  
Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps 7;

Qy 63 STVOEKQONISPLVREGPQVAAHITG-----TRGRSNTLSSPNSKNEKALGRKINS 115

Db 42 SAAQPAHQH-PPKHLAKGTLPAAHLVDGDPSTPDSLRWRANT-----DRAFLR---- 88

Qy 116 WESSRSGHSFLSNLHRLNGELVIEHKGFIYISQTYFRFOEIEIKENTKNDKQMVQYIYKY 175

Db 89 -----HGFL-----LSNNSLLVPTSLGLYFYVSQVVFSGEGCFPKATPTPLVLAHEVQLF 137

Qy 176 TS-YDPDILLMKARNCSWKADEYGLYSYIQGGIFELKENDRIFVSVTNEHLMDHQA 234

Db 138 SSQFPFHVPLLSAQKSCVCPQGPFW-VRSVYQGAFFLLTQGDQLSTHTDGTPLHLLSPSS 196

Qy 235 SFFGAF 240

Db 197 VFFGAF 202

##### RESULT 2

A25451

tumor necrosis factor alpha precursor - rabbit

N/Alternate names: cachectin; TNF alpha

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C/Accession: A25451; J50727

R/Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayaashi, H.;

DNA 5, 149-156, 1986

A/Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabt

A;Reference number: A25454; MUID:86219711; PMID:3519137  
A;Accession: A25454  
A;Molecule type: mRNA  
A;Residues: 1-234 <ITO>  
A;Cross-references: UNIPROT:P04924; GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760  
R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.  
DNA 5, 157-165, 1986  
A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.  
A;Reference number: A25451; MUID:86219712; PMID:3519138  
A;Accession: A25451  
A;Molecule type: DNA  
A;Residues: 1-234 <IT2>  
A;Note: this sequence differs from that shown in having a Gln inserted between residues  
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.  
Gene 95, 215-221, 1990  
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-  
A;Reference number: JH0309; MUID:91065534; PMID:2249779  
A;Accession: JH0727  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-62,'Q',63-234 <SHA>  
A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756  
C;Genetics:  
A;Introns: 62/3; 80/1; 96/1  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; mem  
F;1-81/Domain: propeptide #status predicted <PRO>  
F;82-234/Product: tumor necrosis factor #status predicted <MAT>  
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F;147-178/Disulfide bonds: #status predicted

Query Match 10.2%; Score 131.5; DB 1; Length 234;  
Best Local Similarity 22.9%; Pred. No. 0.00084;  
Matches 50; Conservative 36; Mismatches 79; Indels 53; Gaps 10;

Qy 29 PNDESMNSPCQVQWQLRQLVRKMI-LRTSEETISTVQEQKQINISPLVRERGPQRVAAH 87  
Db 58 PQEESPN-----LHLNVPVQVMTLRSASRALSD-----KEL-----AH 93

Qy 88 ITGTRGSNTLSSPNKNEKALGRKINSWESSRSGHSLNLHLRNGELVTHEKGFYIY 147  
Db 94 VVA-----NPOVEGQL-----QWLSQRANALLANGMKLTDQLVVPADGLYLIY 137

Qy 148 SOTYFRFQEEIKENTKDKQMVQIYKY-TSYPPDILLMKSARNSCKDAEYG-----L 201  
Db 138 SQVLFSGQ-----CGRSVLLTHTVSRFVSPYFNKVNLLSAIKSPCHRETPPEAEPMWY 192

Qy 202 YSIYOGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238  
Db 193 EPIYLGGVFQLEKGDRLSTEVNQPEYLDLAESGQVYFG 230

RESULT 3  
S12606  
tumor necrosis factor alpha precursor - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: S12606; S17290; S18965; I46659  
R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.  
Nucleic Acids Res. 18, 5564, 1990  
A;Title: Gene sequence of porcine tumor necrosis factor alpha.  
A;Reference number: S12606; MUID:91016861; PMID:2216741  
A;Accession: S12606  
A;Molecule type: DNA  
A;Residues: 1-232 <DRE>  
A;Cross-references: UNIPROT:P23563; EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136  
R;Kuhnert, P.; Wuehrlich, C.; Peterhans, E.; Pauli, U.  
Gene 102, 171-178, 1991  
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal  
A;Reference number: S17289; MUID:91340150; PMID:1874444  
A;Accession: S17290  
A;Molecule type: DNA

A;Residues: 1-232 <KU>  
A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134  
A;Note: the authors translated the codon GAG for residue 202 as Gly  
R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.  
submitted to the EMBL Data Library, January 1991  
A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis fac  
A;Reference number: S18965  
A;Accession: S18965  
A;Molecule type: mRNA  
A;Residues: 1-232 <CHO>  
A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138  
R;Pauli, U.; Beutler, B.; Peterhans, E.  
Gene 81, 185-191, 1989  
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction  
A;Reference number: I46659; MUID:90034181; PMID:2478420  
A;Accession: I46659  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: mRNA  
A;Residues: 44-232 <PAU>  
A;Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695  
C;Genetics:  
A;Introns: 62/3; 78/1; 93/1  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myri  
F;1-77/Domain: propeptide #status predicted <PRO>  
F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>  
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F;144-176/Disulfide bonds: #status predicted

Query Match 10.1%; Score 130; DB 1; Length 232;  
Best Local Similarity 25.1%; Pred. No. 0.0011;  
Matches 43; Conservative 30; Mismatches 78; Indels 20; Gaps 6;

Qy 80 GPQVAAHITGTRGSNTLSSPNS---KNEKALGRKINSWESSRSGHSLNLHLRNGEL 136  
Db 66 GPLISINFLAQLGSSSQTSDKPVAAVVAVKAEGQL--QMOSGVANALLANGVKLNQNL 123

Qy 137 VIHEKGFYIYSQTYFRFQEEIKEN---TKNDKQMVQIYKYTSYPPDILLMKSARNSCW 193  
Db 124 VVPDGLYLIYSQVLFVFGQGCPSNTVPLTHTISRIA-----VSYQTKVNLLSAIKSPCQ 177

Qy 194 SK-----DASYGLYSYIYOGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238  
Db 178 RETPEGAERKWPTEPIYLGGVFQLEKDDRLSAEINLPDYLDFAESGQVYFG 228

RESULT 4  
I54490  
tumor necrosis factor alpha precursor - white-footed mouse  
C;Species: Peromyscus leucopus (white-footed mouse)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: I54490  
R;Crew, M.D.; Filipowsky, M.E.  
Immunogenetics 35, 351-353, 1992  
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leuc  
A;Reference number: I54490; MUID:92218012; PMID:1348497  
A;Accession: I54490  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 1-235 <RES>  
A;Cross-references: UNIPROT:P36939; GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507  
C;Genetics:  
A;Gene: P1TNF  
A;Introns: 62/3; 81/1; 97/1  
C;Superfamily: tumor necrosis factor  
C;Keywords: Glycoprotein; lipoprotein; myristylation  
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 10.1%; Score 129.5; DB 2; Length 235;  
Best Local Similarity 24.5%; Pred. No. 0.0013;  
Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;



```
QY 72 ISPLVREGPQVAAHITGTRGRSNTL-SSPNSKNEKALGRKINSWE-----SSRSQH 123
DB 56 IGPOREEFPNNLP--IIGSMAQTTLTRSSSQNSDDKPAHVAVANHQVDEQLEWLSRGN 113
QY 124 SFLSN-LHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIKY-TSYDPP 181
DB 114 ALLANGMDLKNQVLPADGLYLVYSQVLFKQ-----GCSYVLLTHTVSRFAVSIEDK 168
QY 182 ILLMKSARNCSWKDAEYV-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
DB 169 VNLLSAIKSPC-PKETPEGSELKPWYEPYILGGVFOLEKGRLSAEVNLPKYLDPAESGQ 227
QY 236 -PFG 238
DB 228 VYFG 231

RESULT 5
S24641
Lymphotoxin - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: I46046; S24641
R:Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tu
A:Reference number: I46046; MUID:94083525; PMID:8260599
A:Accession: I46046
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-204 <CL2>
A:Cross-references: UNIPROT:Q06600; EMBL:Z14137; NID:g796; PIDN:CAA78510.1; PID:g797
C:Genetics:
A:Introns: 32/3; 68/1
C:Superfamily: tumor necrosis factor

Query Match 9.9%; Score 127.5; DB 1; Length 204;
Best Local Similarity 24.9%; Pred. No. 0.0015;
Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;

QY 61 TISTVQEQKQISPLVRERGPORVAAHITG-----TRGRSNTLSSPNSKNEKALGRKI 113
DB 40 TPSAAQPAHQQL-PTPFRGLTKPANHLVGDPTQDSLRWRANT-----DRAFLR-- 88
QY 114 NSWESSRSRSGHSLNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIY 173
DB 89 -----HGF-----SLSNLSLLVPTSGLYFVYSQVVFSGRCGCPFRATPTPLYLAHEVQ 135
QY 174 KYT-SYDPDILLMKSARNCSWKDAEYGLYSIYQGGIFELKENDRIFVSVTN-EHLIDMD 231
DB 136 LFSPQYPFHVPLLSAQKSCVCPQGPW-VRSYVQAGVFLTRGDQLSTHTDGIHLL-LS 193
QY 232 HEASFFGAP 240
DB 194 PSSVFFGAP 202

RESULT 6
JQ1344
tumor necrosis factor alpha precursor - horse
N:Alternate names: cachectin; TNF alpha
C:Species: Equus caballus (domestic horse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JQ1344
R:Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f
A:Reference number: JQ1344; MUID:92084125; PMID:1748301
A:Accession: JQ1344
A:Molecule type: DNA
A:Residues: 1-234 <SUX>
A:Cross-references: UNIPROT:P29553; GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245
```

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C:Comment: This protein is an important proximal mediator of endotoxemia.
C:Genetics:
A:Gene: TNF-alpha
A:Introns: 62/3; 79/1; 95/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memba
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:146-178/Disulfide bonds: #status predicted

Query Match 9.8%; Score 126; DB 1; Length 234;
Best Local Similarity 22.5%; Pred. No. 0.0025;
Matches 45; Conservative 35; Mismatches 72; Indels 48; Gaps 9;

QY 62 ISTVQEQK-----QNISPLVR-----ERGP-ORVAAHITGTRGRSNTLSSPNSKNEKALG 110
DB 56 IGPOREEQLPNAFQISINPLAQTLRSSSRTPSDKPAHVVA-----NPQAEQ 101
QY 111 RKINSWESSRSGHSLNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQ 170
DB 102 QL--QWLSGRANALLANGVKLTQNLVPLDGLYIYSQVLFKQ-----GCPETH 150
QY 171 YIYKYT-----SYDPDILLMKSARNCSWKDAEYV-----LYSIYQGGIFELKENDRIF 219
DB 151 VLLTHITSLRAVSPSKVNLLSAISKPCHTSPESQAEAKPWYEPYILGGVFOLEKGDQLS 210
QY 220 VSVTNEHLIDMDHEAS-PFG 238
DB 211 AEINQPNVLDPAESGQVYFG 230

RESULT 7
QWUN
tumor necrosis factor alpha precursor [validated] - human
N:Alternate names: cachectin; TNFA
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
C:Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23;
R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.;
Nucleic Acids Res. 13, 6361-6373, 1985
A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chro
A:Reference number: A93585; MUID:86016093; PMID:2995927
A:Accession: A93585
A:Molecule type: DNA
A:Residues: 1-233 <NED>
A:Cross-references: UNIPROT:P01375; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; P;
R:Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka,
Nature Genet. 3, 137-145, 1993
A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A:Reference number: S36152; MUID:93272029; PMID:8499947
A:Accession: S36153
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-233 <IRI>
A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.;
Nature 312, 724-729, 1984
A:Title: Human tumour necrosis factor: precursor structure, expression and homology to 1
A:Reference number: A93351; MUID:85086244; PMID:6392892
A:Accession: A93351
A:Molecule type: mRNA
A:Residues: 1-233 <PEN>
A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A:Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyeloc
R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.;
Science 228, 149-154, 1985
A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A:Reference number: A44189; MUID:85142190; PMID:3856324
A:Accession: A44189
A:Molecule type: mRNA
A:Residues: 1-62, 'S', 64-233 <WAN>
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Lymphokine Res. 7, 175-185, 1988  
A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and  
A:Reference number: A61478; MUID:89301617; PMID:2841543  
A:Accession: A61478  
A:Molecule type: protein  
A:Residues: 56-79;86-95,'X',97,'X',99;119-151,'XX',154-162,'X',164,'X',166,'X',168,'X',1  
R:Voigt, C.G.; Maurer-Poguy, I.; Adolf, G.R.  
FEBS Lett. 314, 85-88, 1992  
A:Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylatic  
A:Reference number: S26951; MUID:93083656; PMID:1451807  
A:Accession: S26951  
A:Molecule type: protein  
A:Residues: 35-59,'N',61-205 <VOI>  
A:Note: 60-Thr was also found  
R:Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.  
Arch. Biochem. Biophys. 304, 144-153, 1993  
A:Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO  
A:Reference number: S34742; MUID:93311995; PMID:8323280  
A:Contents: annotation  
C:Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction,  
while having no detrimental effect on normal cells. It can also act synergistically with  
C:Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of differ  
ical activities but are produced by different cell types and have different induction ki  
C:Genetics:  
A:Gene: GDB:LTA; LT; TNFB  
A:Cross-references: GDB:120442; OMIM:153440  
A:Map position: 6p21.3-6p21.3  
A:Introns: 33/3; 69/1  
A:Note: The first intron occurs before the initiator codon  
C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-205/Product: lymphotoxin #status predicted <MAT>  
F:41/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental  
F:96/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 9.5%; Score 122; DB 1; Length 205;  
Best Local Similarity 23.4%; Pred. No. 0.0046;  
Matches 37; Conservative 29; Mismatches 72; Indels 20; Gaps 5;  
A:Status: preliminary; translated from GB/EMBL/DBJ

Qy 85 AAHTGTGRGNTLSSPNSKNEKALGRKINSWESSRSHSFLSNLHRLNGELVTHEKGFY 144  
Db 64 AAHLIGDSPKNSL-----LWRANTDRAFLQDGFSLNSNLLVPTSIIY 107

Qy 145 YIYSQYTFRPFQBEIKENTKNDKQMVYIYKYTS-YPDPILLMKSARNCSWKDAEYGLYS 203  
Db 108 FVYSQVWFSGRKAYSPKATSSPLLAHEVOLFPSSQYPPHPVLL-SSQKMWYFGLQBPWLHS 166

Qy 204 IYQGGIFELKENDRIFVSVTN-EHLMDHREASFGAF 240  
Db 167 MYHGAAFOLQGDQLSTHTDGIPLHLV-LSPSTVFEGAF 203

RESULT 9  
QWMSN  
tumor necrosis factor alpha precursor - mouse  
N:Alternate names: cachectin; TNF alpha  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 09-Jul-2004  
C:Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696  
R:Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.  
DNA 7, 193-201, 1988  
A:Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis  
A:Reference number: A22908; MUID:89224564; PMID:2836146  
A:Accession: A22908  
A:Molecule type: DNA  
A:Residues: 1-235 <SHI>  
A:Cross-references: UNIPROT:P06804; GB:M20155  
R:Shakhov, A.N.; Nedospasov, S.A.  
Bioorg. Khim. 13, 701-705, 1987  
A:Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucl  
A:Reference number: S03791; MUID:87298639; PMID:3040015  
A:Accession: S03791

A:Molecule type: DNA  
A:Residues: 1-235 <SHA>  
A:Cross-references: GB:M38296; NID:g202086; PIDN:AAA040459.1; PID:g202087  
R:Note: article in Russian with English abstract  
R:Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.  
Nucleic Acids Res. 15, 9083-9084, 1987  
A:Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor necr  
A:Reference number: A93679; MUID:88067722; PMID:368454  
A:Accession: A27303  
A:Molecule type: DNA  
A:Residues: 1-235 <SEM>  
A:Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832  
R:Pennica, D.; Hayflick, J.S.; Bringham, T.S.; Palladino, M.A.; Goeddel, D.V.  
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985  
A:Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis  
A:Reference number: A25164; MUID:85298296; PMID:3898078  
A:Accession: A25164  
A:Molecule type: mRNA  
A:Residues: 1-235 <PEN>  
A:Cross-references: GB:M11731; NID:g202084; PIDN:AAA040458.1; PID:g202085  
R:Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima, I  
Nucleic Acids Res. 13, 4417-4429, 1985  
A:Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expres  
A:Reference number: A23127; MUID:85242112; PMID:2989794  
A:Accession: A23127  
A:Molecule type: mRNA  
A:Residues: 1-235 <FRA>  
A:Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845  
R:Cseh, K.; Beutler, B.  
J. Biol. Chem. 264, 16256-16260, 1989  
A:Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results i  
A:Reference number: A34251; MUID:89380231; PMID:2777790  
A:Accession: A34251  
A:Molecule type: protein  
A:Residues: 70-87 <CSB>  
R:Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986  
A:Title: Identification of a common nucleotide sequence in the 3'-untranslated region of  
A:Reference number: I59058; MUID:86149365; PMID:2419912  
A:Accession: I59058  
A:Status: preliminary; translated from GB/EMBL/DBJ

Query Match 9.4%; Score 121; DB 1; Length 235;  
Best Local Similarity 23.1%; Pred. No. 0.0066;  
Matches 43; Conservative 34; Mismatches 79; Indels 30; Gaps 8;  
A:Status: preliminary; translated from GB/EMBL/DBJ

Qy 67 EKQONI SPLVRERGFQVAAHITGRGRSNTLSP-----NSKNEKALGRKINSWESSR 120  
Db 62 EKFPNGLPLI-----SSMAQTLTLRSSSQNSSDKPFVAVHVAHQVEQL-----EWSOR 111

Qy 121 SGHSFLSNLHRLNGELVTHEKGFFVYSQYFRFQEEIKENTKNDKQMVYIYKYT-SYP 179  
Db 112 ANALLANGMDLKNQLNQLVVPADGLVLYVSQVLFKQ-----GCPDVLVLTHTVSRPAISYQ 166

Qy 180 DPTLLMKSARNSCWSDAEYG-----LYSYIQGIGELKENDRIFYSVTNEHLIDMDHE 233  
Db 167 EKNVLUSAVSPC-PRDTPEGAELKPWTYEPYLGGVFQLEKGDLQSAEVLNPKYLDFASS 225

Qy 234 AS-FFG 238  
Db 226 GOVYFG 231

RESULT 10

JU0029

tumor necrosis factor alpha precursor - rat

N;Alternate names: cachectin; TNF alpha

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #text\_change 09-Jul-2004

C;Accession: JU0029; JN0868; S21674

R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.

Agric. Biol. Chem. 53, 1733-1736, 1989

A;Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis factor

A;Reference number: JU0029

A;Accession: JU0029

A;Molecule type: DNA

A;Residues: 1-235 <SH1>

A;Cross-references: UNIPROT:P16599

R;Kwon, J.; Chung, I.Y.; Benveniste, E.N.

Gene 132, 227-236, 1993

A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.

A;Residues: 1-235 <KWO>  
A;Cross-references: GB:I00981; NID:G205253; PIDN:AAAL6275.1; PID:G205254  
R;Estler, H.C.; Grewe, M.; Gausling, R.; Pavlovic, M.; Decker, K.  
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992  
A;Title: Rat tumor necrosis factor- $\alpha$ . Transcription in rat Kupffer cells and in vitro  
A;Reference number: S21674; MUID:92329007; PMID:1627266  
A;Accession: S21674  
A;Molecule type: mRNA  
A;Residues: 1-38, 'P', 40-162, 'T', 164-201, 'S', 203-235 <EST>  
A;Cross-references: GB:X66539; GB:S40199; NID:G395369; PIDN:CAA47146.1; PID:G395370  
C;Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and  
C;Genetics:  
A;Gene: TNF- $\alpha$   
A;Introns: 62/3; 81/1; 97/1  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; mem  
F;80-235/Product: tumor necrosis factor #status predicted <NAI>  
F;19,20/Binding site: myristate (lys) (covalent) #status predicted  
F;84/Binding site: carboxylate (Ser) (covalent) #status predicted  
F;86/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;148-179/Disulfide bonds: #status predicted

[illegible]

RESULT 11  
S22052  
tumor necrosis factor alpha precursor - baboon  
C:Species: Papio sp. (baboon)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S22052  
R:Sanjanwala, M.; Edwards, A.  
submitted to the EMBL Data Library, September 1991  
A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.  
A:Reference number: S22052  
A:Accession: S22052  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-233 <SAN>  
A:Cross-references: UNIPROT:P33620; EMBL:X62141; NID:G38159; PIDN:CAA44068.1; PID:G38160  
C:Genetics:  
A:Introns: 62/3; 78/1; 94/1  
C:Superfamily: tumor necrosis factor  
C:Keywords: Glycoprotein; lipoprotein; myristylation; transmembrane protein  
F:19,20/Binding site: myristate (lys) (covalent) #status predicted  
F:81/Binding site: carbohydrate (ser) (covalent) #status predicted  
F:145-177/Disulfide bonds: #status predicted

[illegible]

RESULT 12

JH0529  
tumor necrosis factor alpha precursor - sheep  
N;Alternate names: cachectin; TNF alpha  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: JH0529; S48118; S13114; S20661  
R;Green, I.R.; Sargan, D.R.  
Gene 109, 203-210, 1991  
A;Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with  
A;Reference number: JH0529; MUID:92112044; PMID:1765267  
A;Accession: JH0529  
A;Molecule type: mRNA  
A;Residues: 1-234 <GRE>  
A;Cross-references: UNIPROT:P23383; EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406  
A;Experimental source: alveolar macrophage  
R;Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.  
Immunol. Cell Biol. 69, 273-283, 1991  
A;Title: Molecular cloning, expression and characterization of ovine TNF-alpha.  
A;Reference number: S48118; MUID:92155784; PMID:1786996  
A;Accession: S48118  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-234 <NAS>  
A;Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807  
R;Young, A.J.; Hay, J.B.; Chan, J.Y.C.  
Nucleic Acids Res. 18, 6723, 1990  
A;Title: Primary structure of ovine tumor necrosis factor alpha cDNA.

A:Reference number: S13114; MUID:91067496; PMID:2251151

A:Accession: S13114

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-62,64-234 <YOU>

A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A:Note: comparison with the introns of homologous sequences suggest that this is probably

C:Superfamily: tumor necrosis factor

C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lympho

F:1-77/Domain: propeptide #status predicted <PRO>

F:20/Binding site: myristate (Lys) (covalent) #status predicted <TUM>

F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:146-178/disulfide bonds: #status predicted

Query Match 9.1%; Score 117.5; DB 1; Length 234;

Best Local Similarity 23.0%; Pred. No. 0.013;

Matches 42; Conservative 30; Mismatches 78; Indels 33; Gaps 7;

Qy 80 GPQRVAHITG---TRGRSNTL-GSPNSKNKALGRKINS-----WESSRSGHSFLS 127

Db 57 GPQREQSPAGPSFNRLVQLTSSQASNNKPVAVHVNISAPQLRWGDSYANALMAN 116

Qy 128 NLHLRNGELVTHKEGFYIYSQYVRFQOEIKENTKNDKQMVQIYKYT-----SYDDP 181

Db 117 GVLEKQNLQVPTDGLYLIYSQVLF-----GHGCPSTPLFLTHTSIRIAVSYQTK 167

Qy 182 ILLMKARNSCWSK-----DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEAS- 235

Db 168 VNIILSAIKSPCHRETLGAEAKPWYPIYQGGVQLEKGRDLRSAINLPEYLDVAESQV 227

Qy 236 FFG 238

Db 228 YFG 230

RESULT 13

S06192

tumor necrosis factor alpha precursor - goat (fragment)

N:Alternate names: cachectin; TNF alpha

C:Species: Capra aegagrus hircus (domestic goat)

C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004

C:Accession: S06192; S41867

R:Goldstein, I.M.; Henner, D.; Talhouk, A.

submitted to the EMBL Data Library, March 1989

A:Reference number: S06192

A:Accession: S06192

A:Molecule type: mRNA

A:Residues: 1-193 <GOL>

A:Cross-references: UNIPROT:P13296; EMBL:X14828; NID:g992; PIDN:CAA32937.1; PID:g993

R:Rimstad, E.

submitted to the EMBL Data Library, January 1994

A:Reference number: S41867

A:Accession: S41867

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 36-38,'S',40-78,'A',80-88,'N',90-114,'Q',116-123,'D',125-144,'G',145-173,'L'

A:Cross-references: EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PID:g452608

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane protein

F:42/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:106-138/disulfide bonds: #status predicted

Query Match 9.0%; Score 115.5; DB 2; Length 193;

Best Local Similarity 20.4%; Pred. No. 0.015;

Matches 45; Conservative 36; Mismatches 79; Indels 61; Gaps 9;

Qy 29 PNDESNMSPQVQKQWLKRVKMLRTSBETISTTQEQKQNTSPLVRERGPKQVAAHI 88

Db 19 PEEQSPAGPSFN-----RPLVQ--TLASSSQASS-----NKPVAHV 53

Qy 89 TGTRGRSNTLSPNSKNKALGRKINSWESSRSGHSFLSNLHLRNGELVTHKEGFYIYS 148

A:Reference number: S13114; MUID:91067496; PMID:2251151

A:Accession: S13114

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-62,64-234 <YOU>

A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A:Note: comparison with the introns of homologous sequences suggest that this is probably

C:Superfamily: tumor necrosis factor

C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lympho

F:1-77/Domain: propeptide #status predicted <PRO>

F:20/Binding site: myristate (Lys) (covalent) #status predicted <TUM>

F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:146-178/disulfide bonds: #status predicted

Query Match 9.1%; Score 117.5; DB 1; Length 234;

Best Local Similarity 23.0%; Pred. No. 0.013;

Matches 42; Conservative 30; Mismatches 78; Indels 33; Gaps 7;

Qy 80 GPQRVAHITG---TRGRSNTL-GSPNSKNKALGRKINS-----WESSRSGHSFLS 127

Db 57 GPQREQSPAGPSFNRLVQLTSSQASNNKPVAVHVNISAPQLRWGDSYANALMAN 116

Qy 128 NLHLRNGELVTHKEGFYIYSQYVRFQOEIKENTKNDKQMVQIYKYT-----SYDDP 181

Db 117 GVLEKQNLQVPTDGLYLIYSQVLF-----GHGCPSTPLFLTHTSIRIAVSYQTK 167

Qy 182 ILLMKARNSCWSK-----DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEAS- 235

Db 168 VNIILSAIKSPCHRETLGAEAKPWYPIYQGGVQLEKGRDLRSAINLPEYLDVAESQV 227

Qy 236 FFG 238

Db 228 YFG 230

RESULT 13

S06192

tumor necrosis factor alpha precursor - goat (fragment)

N:Alternate names: cachectin; TNF alpha

C:Species: Capra aegagrus hircus (domestic goat)

C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004

C:Accession: S06192; S41867

R:Goldstein, I.M.; Henner, D.; Talhouk, A.

submitted to the EMBL Data Library, March 1989

A:Reference number: S06192

A:Accession: S06192

A:Molecule type: mRNA

A:Residues: 1-193 <GOL>

A:Cross-references: UNIPROT:P13296; EMBL:X14828; NID:g992; PIDN:CAA32937.1; PID:g993

R:Rimstad, E.

submitted to the EMBL Data Library, January 1994

A:Reference number: S41867

A:Accession: S41867

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 36-38,'S',40-78,'A',80-88,'N',90-114,'Q',116-123,'D',125-144,'G',145-173,'L'

A:Cross-references: EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PID:g452608

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane protein

F:42/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:106-138/disulfide bonds: #status predicted

Query Match 9.0%; Score 115.5; DB 2; Length 193;

Best Local Similarity 20.4%; Pred. No. 0.015;

Matches 45; Conservative 36; Mismatches 79; Indels 61; Gaps 9;

Qy 29 PNDESNMSPQVQKQWLKRVKMLRTSBETISTTQEQKQNTSPLVRERGPKQVAAHI 88

Db 19 PEEQSPAGPSFN-----RPLVQ--TLASSSQASS-----NKPVAHV 53

Qy 89 TGTRGRSNTLSPNSKNKALGRKINSWESSRSGHSFLSNLHLRNGELVTHKEGFYIYS 148

A:Reference number: S13114; MUID:91067496; PMID:2251151

A:Accession: S13114

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-62,64-234 <YOU>

A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A:Note: comparison with the introns of homologous sequences suggest that this is probably

C:Superfamily: tumor necrosis factor

C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lympho

F:1-77/Domain: propeptide #status predicted <PRO>

F:20/Binding site: myristate (Lys) (covalent) #status predicted <TUM>

F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:146-178/disulfide bonds: #status predicted

Query Match 9.1%; Score 117.5; DB 1; Length 234;

Best Local Similarity 23.0%; Pred. No. 0.013;

Matches 42; Conservative 30; Mismatches 78; Indels 33; Gaps 7;

Qy 80 GPQRVAHITG---TRGRSNTL-GSPNSKNKALGRKINS-----WESSRSGHSFLS 127

Db 57 GPQREQSPAGPSFNRLVQLTSSQASNNKPVAVHVNISAPQLRWGDSYANALMAN 116

Qy 128 NLHLRNGELVTHKEGFYIYSQYVRFQOEIKENTKNDKQMVQIYKYT-----SYDDP 181

Db 117 GVLEKQNLQVPTDGLYLIYSQVLF-----GHGCPSTPLFLTHTSIRIAVSYQTK 167

Qy 182 ILLMKARNSCWSK-----DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEAS- 235

Db 168 VNIILSAIKSPCHRETLGAEAKPWYPIYQGGVQLEKGRDLRSAINLPEYLDVAESQV 227

Qy 236 FFG 238

Db 228 YFG 230

RESULT 13

S06192

tumor necrosis factor alpha precursor - goat (fragment)

N:Alternate names: cachectin; TNF alpha

C:Species: Capra aegagrus hircus (domestic goat)

C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004

C:Accession: S06192; S41867

R:Goldstein, I.M.; Henner, D.; Talhouk, A.

submitted to the EMBL Data Library, March 1989

A:Reference number: S06192

A:Accession: S06192

A:Molecule type: mRNA

A:Residues: 1-193 <GOL>

A:Cross-references: UNIPROT:P13296; EMBL:X14828; NID:g992; PIDN:CAA32937.1; PID:g993

R:Rimstad, E.

submitted to the EMBL Data Library, January 1994

A:Reference number: S41867

A:Accession: S41867

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 36-38,'S',40-78,'A',80-88,'N',90-114,'Q',116-123,'D',125-144,'G',145-173,'L'

A:Cross-references: EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PID:g452608

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane protein

F:42/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:106-138/disulfide bonds: #status predicted

Query Match 9.0%; Score 115.5; DB 2; Length 193;

Best Local Similarity 20.4%; Pred. No. 0.015;

Matches 45; Conservative 36; Mismatches 79; Indels 61; Gaps 9;

Qy 29 PNDESNMSPQVQKQWLKRVKMLRTSBETISTTQEQKQNTSPLVRERGPKQVAAHI 88

Db 19 PEEQSPAGPSFN-----RPLVQ--TLASSSQASS-----NKPVAHV 53

Qy 89 TGTRGRSNTLSPNSKNKALGRKINSWESSRSGHSFLSNLHLRNGELVTHKEGFYIYS 148

A:Reference number: S13114; MUID:91067496; PMID:2251151

A:Accession: S13114

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-62,64-234 <YOU>

A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A:Note: comparison with the introns of homologous sequences suggest that this is probably

C:Superfamily: tumor necrosis factor

C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lympho

F:1-77/Domain: propeptide #status predicted <PRO>

F:20/Binding site: myristate (Lys) (covalent) #status predicted <TUM>

F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:146-178/disulfide bonds: #status predicted

Query Match 9.1%; Score 117.5; DB 1; Length 234;

Best Local Similarity 23.0%; Pred. No. 0.013;

Matches 42; Conservative 30; Mismatches 78; Indels 33; Gaps 7;

Qy 80 GPQRVAHITG---TRGRSNTL-GSPNSKNKALGRKINS-----WESSRSGHSFLS 127

Db 57 GPQREQSPAGPSFNRLVQLTSSQASNNKPVAVHVNISAPQLRWGDSYANALMAN 116

Qy 128 NLHLRNGELVTHKEGFYIYSQYVRFQOEIKENTKNDKQMVQIYKYT-----SYDDP 181

Db 117 GVLEKQNLQVPTDGLYLIYSQVLF-----GHGCPSTPLFLTHTSIRIAVSYQTK 167

Qy 182 ILLMKARNSCWSK-----DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEAS- 235

Db 168 VNIILSAIKSPCHRETLGAEAKPWYPIYQGGVQLEKGRDLRSAINLPEYLDVAESQV 227

Qy 236 FFG 238

Db 228 YFG 230

RESULT 13

S06192

tumor necrosis factor alpha precursor - goat (fragment)

N:Alternate names: cachectin; TNF alpha

C:Species: Capra aegagrus hircus (domestic goat)

C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004

C:Accession: S06192; S41867

R:Goldstein, I.M.; Henner, D.; Talhouk, A.

submitted to the EMBL Data Library, March 1989

A:Reference number: S06192

A:Accession: S06192

A:Molecule type: mRNA

A:Residues: 1-193 <GOL>

[illegible]

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2005, 06:15:49 ; Search time 40 Seconds  
(without alignments)  
675.923 Million cell updates/sec

Title: US-10-662-431-2  
Perfect score: 1478  
Sequence: 1 MAMMEVGGSLGTCVLIIV.....NEHLIDMDHEASFFGAFVVG 281

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: Pirl1:\*  
2: Pirl2:\*  
3: Pirl3:\*  
4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189.5	12.8	279	2 A53062	Fas ligand - mouse
2	186	12.6	281	2 I38707	Fas ligand - human
3	177.5	12.0	278	2 A49266	fas ligand - rat
4	164	11.1	261	2 S53090	CD40 ligand - bovi
5	147.5	10.0	261	2 I53476	CD40 ligand - huma
6	141	9.5	234	1 A25451	tumor necrosis fac
7	141	9.5	260	2 S21738	CD40 ligand - mous
8	134.5	9.1	204	1 S17289	tumor necrosis fac
9	133	9.0	232	1 S12606	tumor necrosis fac
10	131.5	8.9	233	1 S22052	tumor necrosis fac
11	131	8.9	234	1 J01344	tumor necrosis fac
12	130.5	8.8	233	1 S24642	tumor necrosis fac
13	129.5	8.8	235	2 I54490	tumor necrosis fac
14	127.5	8.6	204	1 S24641	lymphotoxin - bovi
15	125.5	8.5	233	1 QWUN	tumor necrosis fac
16	123.5	8.4	235	1 QWNSN	tumor necrosis fac
17	123.5	8.4	235	2 JU0029	tumor necrosis fac
18	122	8.3	205	1 QHUX	lymphotoxin alpha
19	121	8.2	234	1 QH0529	tumor necrosis fac
20	115.5	7.8	193	2 S06192	tumor necrosis fac
21	114	7.7	202	1 B27303	tumor necrosis fac
22	113.5	7.7	185	2 S22715	tumor necrosis fac
23	113.5	7.7	306	2 I4912M	lymphotoxin-beta -
24	112.5	7.6	638	1 QQBY2M	mRNA maturase b14
25	111.5	7.5	202	1 JN0869	tumor necrosis fac
26	109	7.4	652	2 I48083	amphotropic murine
27	107	7.2	197	1 JH0309	tumor necrosis fac
28	102	6.9	244	2 A46066	lymphotoxin beta -
29	100	6.8	865	2 A81658	probable membrane

30 99.5 6.7 233 2 S11688 tumor necrosis fac  
31 97.5 6.6 448 2 F95122 protein kinase, pr  
32 95 6.4 345 2 T14707 DNA ligase homolog  
33 95 6.4 365 2 T15010 hypothetical prote  
34 95 6.4 455 2 G95104 hypothetical prote  
35 94.5 6.4 4981 2 T18489 hypothetical prote  
36 94 6.4 1465 2 T23056 chromodomain helic  
37 92.5 6.3 833 1 A31593 heat shock transcr  
38 92.5 6.3 1538 2 T29095 cardiac muscle fac  
39 91 6.2 1176 2 JN0583 myosin-light-chain  
40 90.5 6.1 502 2 JC2491 serine/threonine k  
41 90.5 6.1 502 2 A53444 actinin receptor-1  
42 90.5 6.1 1284 2 T40578 hypothetical prote  
43 90 6.1 907 2 E96636 hypothetical prote  
44 89.5 6.1 313 2 T03031 NBS-LRR type resis  
45 89 6.0 328 2 B59296 alpha-N-arabinofur

ALIGNMENTS

RESULT 1  
A53062  
Fas ligand - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: A53062  
R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag  
Cell 76, 969-976, 1994  
A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in t  
A;Reference number: A53062; MUID:94185175; PMID:7511063  
A;Accession: A53062  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-279 <TAK>  
A;Cross-references: UNIPROT:P41047; GB:U06948; NID:g473564; PIDN:AAAL7800.1; PID:g473565

Query Match 12.8%; Score 189.5; DB 2; Length 279;  
Best Local Similarity 25.8%; Pred. No. 1.7e-08;  
Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;

Qy 83 QLRQLVKAMLTSEETISTVQEKQNLSPVLRGPGORVAHLITGTRGNTLSSPNK 142  
Db 111 ELREFTNQSL-----KVSSFQKQIANPSTPEKKPRSV-AHLTG-----NPHSR 154  
Qy 143 NEKALGRKINSWSSRSGHSLNHLRNGELVTHEKGFYIYSQTYRFOEIKENTKN 202  
Db 155 SIPL-----EWEDT-YGTALISGVKKYKGGVLINETGLYFVYSKVYFRGQ-----SCN 201  
Qy 203 DKQWQVIY-KYTSYDPDILLMSAR-NSCWKDAEYGLYSIYOGGIFELKENDRIFVSV 260  
Db 202 NQPLNHKVYMRNSKYPEDLVLMEEKRLNYCTT--GQIWAHSSYLGAVFNLTSADHLVYNI 259  
Qy 261 TNEHLIDMDHEASFFGAF 278  
Db 260 SQLSLINFESKTFFGLY 277

RESULT 2  
I38707  
Fas ligand - human  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: I38707; JC2340; S57565; I38554  
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.  
Int. Immunol. 6, 1567-1574, 1994  
A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity.  
A;Reference number: I38707; MUID:95127560; PMID:7826947  
A;Accession: I38707  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-281 <RES>  
A;Cross-references: UNIPROT:P48023; EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g59543

R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Biochem. Biophys. Res. Commun. 204, 468-474, 1994  
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.  
A;Reference number: JC2340; MUID:95071350; PMID:7980502  
A;Accession: JC2340  
A;Molecule type: DNA  
A;Residues: 1-281 <MIT>  
A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g1369902  
R;Schatzlein, C.E.  
submitted to the EMBL Data Library, June 1995  
A;Reference number: S57565  
A;Accession: S57565  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-281 <SCH>  
A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456  
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; Gc J. Exp. Med. 181, 71-77, 1995  
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.  
A;Reference number: I38554; MUID:95105731; PMID:7528780  
A;Accession: I38554  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-281 <RE2>  
A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628  
C;Genetics:  
A;Gene: FasL  
A;Introns: 151/1; 116/3  
A;Keywords: Glycoprotein; transmembrane protein  
F;80-102/Domain: transmembrane #status predicted <TMM>  
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 186; DB 2; Length 281;  
Best Local Similarity 22.1%; Pred. No. 3.4e-08;  
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;

Qy 4 MEVQGGPSLQTCVLIVFTLLQSLCVAV---FYVFTNELKQMDQKYSKGIACFLKE 60  
Db 71 LKRGHNSTG-LCLLVMFVVALVGLGMFQLPHLQELAELESTQMHFTASSLEK 129  
Qy 61 DDSVWDNDDESMNSPCQVQWQRLQRLVRKMLRTSETISTVQEKQONISPLVRGPQ 120  
Db 130 QIGHPSPPPE-----KKELRKV----- 146  
Qy 121 RVAAHITGRGSRNTLSSPNKNEKALGRKINSWESSRSGHSPSLNHLRNGELVIEHGK 180  
Db 147 ---AHLT---GKSNRSM-----LEWEDT-YGIVLUSGVKYKGGGLVINEGT 187  
Qy 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIY-KYTSYDPDPILLMKSARNS-----CWSK 233  
Db 188 LYPVYSKVYFRGQ-----SCNNLPLSHKVYMRNSKYPQDLVWMEGKMWSCYTTGQMWAR 241  
Qy 234 DAEGVLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPFGAF 278  
Db 242 -----SSYLGVFNLTSADHLVYVNSLSLVNFEESQTFPGLY 279

RESULT 3  
A49266  
fas ligand - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: A49266  
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.  
Cell 75, 1169-1178, 1993  
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor gene family.  
A;Reference number: A49266; MUID:94084792; PMID:7505205  
A;Accession: A49266  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-278 <SUD>  
A;Cross-references: UNIPROT:P36940; GB:U03470; NID:g440179; PIDN:AAC52129.1; PID:g440179  
C;Keywords: Glycoprotein; transmembrane protein

Query Match 12.0%; Score 177.5; DB 2; Length 278;  
Best Local Similarity 27.5%; Pred. No. 1.8e-07;  
Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

Qy 100 ISTVQEKQONISPLVRERGPORVAAHITGT-RGRSNTLSSPNKNEKALGRKINSWESSR 158  
Db 121 VSSFEKQIANPSTPSETKKPRSV-AHLTGNPRSRSIPL-----EWEDT- 162  
Qy 159 SCHSFLSNLHRLNGELVIEHKGFYIYSQTYFRFOBEIKENTKNDKQMVQYIY-KYTSYP 217  
Db 163 YGTALISGVKYKGGGLVINEAGLYFYYSKVYFRGQ-----SCNSQPLSHKVYMRNFKYP 216  
Qy 218 DPILLMKSAR-NSCWSKDAEYGLYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPFG 276  
Db 217 GDVLMEKKLNLYCTT---GGIWAHSSVILGAVNLTVADHLVYVNSLSLINFESKTFPG 274  
Qy 277 AF 278  
Db 275 LY 276

RESULT 4  
S53090  
CD40 ligand - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C;Accession: S53090  
R;Mertens, B.E.L.C.; Muriuki, M.  
submitted to the EMBL Data Library, February 1995  
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.  
A;Reference number: S53090  
A;Accession: S53090  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-261 <MER>  
A;Cross-references: UNIPROT:P51749; EMBL:Z48469; NID:g732569; PIDN:CAA88363.1; PID:g7325;

Query Match 11.1%; Score 164; DB 2; Length 261;  
Best Local Similarity 25.9%; Pred. No. 2.3e-06;  
Matches 72; Conservative 52; Mismatches 114; Indels 40; Gaps 14;

Qy 6 VQGGPSLQTCVLIVFTVLL--QSLCAVAVYVYFTNELKQMDQKYSKGIACFLKEDDS 63  
Db 13 VATGPPVSMK-IFMYLLTVFLITQMGSAFVAVLHRLDKIEDERNLHEDFVFMK---T 68  
Qy 64 YWPDNEESMNS--PCWQVQWQRLQRLVRKMLRTSETISTVQEKQONISPLVRERGPQ 121  
Db 69 IQRCNKGGSLNLCNCEIRSRFEDLV-KDIMQNK-----VKKEKNFEMHKGQDQBPQ- 121  
Qy 122 VAAHITGRGSRNTLSSPNKNEKALGRKINSWESSRSGHSPSLN--LHLRNG-ELVIEH 178  
Db 122 IAAHV-----ISEASKTTSVL-----QW--APKGYTSLNNLVTLENGQLAVKR 165  
Qy 179 KGFYIYSQTYFRFOBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEY 238  
Db 166 QGFYIYVTVTFCSNR---TLQAPFIASLCLKSPSGSERILLRAANTHSSSKPC-G 219  
Qy 239 LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPFG 276  
Db 220 QQSIHLGGVFELOSGASVFNVTDPQSVSHGTGFTSFG 257

RESULT 5  
I53476  
CD40 ligand - human  
N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: S28017; JH0793; S28852; I53476; S25684; S30593  
R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; EMBO J. 11, 4313-4321, 1992  
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for



A;Reference number: S28017; MUID:93049181; PMID:1385114  
A;Accession: S28017  
A;Molecule type: mRNA  
A;Residues: 1-261 <HOL>  
A;Cross-references: UNIPROT:P29965; EMBL:Z15017; NID:G38483; PIDN:CAA78737.1; PID:G38484  
R;Striggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.  
J. Exp. Med. 176, 1543-1550, 1992  
A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin  
A;Reference number: JH0793; MUID:93094757; PMID:1281209  
A;Accession: JH0793  
A;Molecule type: mRNA  
A;Residues: 1-261 <SPR>  
A;Cross-references: GB:X67878; NID:G38411; PIDN:CAA48077.1; PID:G38412  
R;Graf, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Krocsek, R.A.  
Eur. J. Immunol. 22, 3191-3194, 1992  
A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.  
A;Reference number: S26694; MUID:93076854; PMID:1280226  
A;Accession: S26694  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-261 <GRA>  
A;Cross-references: EMBL:X68550; NID:G37269; PIDN:CAA48554.1; PID:G37270  
R;Gauchat, J.P.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.  
FEBS Lett. 315, 259-266, 1993  
A;Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e  
A;Reference number: S28852; MUID:93138085; PMID:7678552  
A;Accession: S28852  
A;Molecule type: mRNA  
A;Residues: 1-261 <GAU>  
A;Cross-references: EMBL:L07414; NID:G180123; PIDN:AAA35662.1; PID:G180124  
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln  
C;Genetics:  
A;Gene: GDB:CD40LG; HIGM1; IMD3  
A;Map position: Xq26-Xq26  
A;Keywords: glycoprotein; transmembrane protein  
F;13-44/Domain: transmembrane #status predicted <TM>  
F;45-261/Domain: extracellular #status predicted <EXT>  
F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.0%; Score 147.5; DB 2; Length 261;  
Best Local Similarity 23.7%; Pred. No. 5.7e-05;  
Matches 66; Conservative 51; Mismatches 99; Indels 63; Gaps 15;

Qy 17 VLIVFTLL--QSLCAVTVVYFTNELKQMDKYSKGIACFLKEDDSYWDP-----ND 69  
Db 23 IFVLLTVFLITQMGSLFAVYLLHRLDKLIEDRN-----LHEDVFVKTQRCNTG 75  
Qy 70 EESMN-SFCWQVQWLRLVRKMLRTSEETISTVQEQKQNSPLVRERGQPVAAHITG 128  
Db 76 ERSLLNCEBIKQFEGFVKDML-NKEET-----KKENSFEMQKGDQNPQ-IAAHV-- 126  
Qy 129 TRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSN--LHLNG-ELVTHEKGFYIY 185  
Db 127 -----ISEASKTTSVL-----QW--AEKGYTMSNNVLTENGKOLTVKRQGLYIY 172  
Qy 186 SQTFRFOEIKENT-----KNDKQMVQYIKYTSYPPDPIILMKSNCSWKSQAEY 237  
Db 173 AQVTFCSNREASSQAPFTASICLSPGRFR-----ILLRANTHSSAKPC-- 218  
Qy 238 GLYSIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276  
Db 219 GQSIHLGGVPELQGSVFNVTDPQSQVSHGTGFTSGF 257

RESULT 6  
A25451  
tumor necrosis factor alpha precursor - rabbit  
N;Alternate names: cachectin; TNF alpha  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: A25451; JS0729

R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayaashi, H.;  
DNA 5, 149-156, 1986  
A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabt  
A;Reference number: A25454; MUID:86219711; PMID:3519137  
A;Accession: A25454  
A;Molecule type: mRNA  
A;Residues: 1-234 <ITO>  
A;Cross-references: UNIPROT:P04924; GB:M12845; NID:G165759; PIDN:AAA31486.1; PID:G165760  
R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Jongeneel, C.V.; Nedospasov, S.A.  
DNA 5, 157-165, 1986  
A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.  
A;Reference number: A25451; MUID:86219712; PMID:3519138  
A;Accession: A25451  
A;Molecule type: DNA  
A;Residues: 1-234 <IT2>  
A;Note: this sequence differs from that shown in having a Gln inserted between residues (e  
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.  
Gene 95, 215-221, 1990  
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-1  
A;Reference number: JH0309; MUID:91065534; PMID:2249779  
A;Accession: JS0727  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-62,'Q' 63-234 <SHA>  
A;Cross-references: GB:M60340; GB:M35326; NID:G165754; PIDN:AAA31484.1; PID:G165756  
C;Genetics:  
A;Introns: 62/3; 80/1; 96/1  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membi  
F;1-81/Domain: propeptide #status predicted <PRO>  
F;82-234/Product: tumor necrosis factor #status predicted <MAT>  
F;19,20/Binding site: myristate (lys) (covalent) #status predicted  
F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F;147-178/Disulfide bonds: #status predicted

Query Match 9.5%; Score 141; DB 1; Length 234;  
Best Local Similarity 22.4%; Pred. No. 0.00017;  
Matches 62; Conservative 41; Mismatches 98; Indels 76; Gaps 13;

Qy 8 GGPSLGTCVLIVFTLLQSLCAVTVVYFTNELKQMDKYSKGIACFLKEDDSYWDP 67  
Db 22 GGPGSKRCLCLSLFSLFLL---VAGATTLF-----CLL--HFRVIGP 58  
Qy 68 NDESMNSPCWQVQWLRLVRKMLRTSEETISTVQEQKQNSPLVRERGQPVAAHI 126  
Db 59 QEEESPNN-----LHLVNPVQMVTLRSASRLSD-----KPL-----AHV 94  
Qy 127 TGTRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHLRNGELVTHEKGFYIYS 186  
Db 95 VA-----NPQVEGQL-----QWLSORANALLANGMKUTDQLVVPADGLYIYS 138  
Qy 187 QTYFRFOEIKENTKNDKQMVQYIKYTSYPPDPIILMKSNCSWKSQAEYG-----LY 240  
Db 139 QVLFSGQ-----GCRSYVLLTHTVSRFAVSYPYKVNLLSAIKSPCHRETPAEAPMAYE 193  
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEAS-PPG 276  
Db 194 PVLGGVFLQLEKGRDLSTEVNQPEYLDLAEISGVYFG 230

RESULT 7  
S21738  
CD40 ligand - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: S21738  
R;Armitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, B.N.  
; Cosman, D.; Spriggs, M.K.  
Nature 357, 80-82, 1992  
A;Title: Molecular and biological characterization of a murine ligand for CD40.  
A;Reference number: S21738; MUID:92244364; PMID:1374165  
A;Accession: S21738  
A;Molecule type: mRNA



```
Dh 182 EGAERKPYEPIYLGGVFQLEKDRLSAEINLPDYLDFAESGQVYFG 228
RESULT 10
S22052
tumor necrosis factor alpha precursor - baboon
C:Species: Papio sp. (baboon)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S22052
R:Sanjanwala, M.; Edwards, A.
A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A:Reference number: S22052
A:Accession: S22052
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <SAN>
A:Cross-references: UNIPROT:P33620; EMBL:X62141; NID:G38159; PIDN:CAA44068.1; PID:G38160
C:Genetics:
A:Introns: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:19/20/Binding site: myristate (Lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted
Query Match 8.9%; Score 131.5; DB 1; Length 233;
Best Local Similarity 19.2%; Pred. No. 0.0011;
Matches 55; Conservative 49; Mismatches 98; Indels 85; Gaps 10;
Qy 2 AMMEVQGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKED 61
Dh 16 ALPKTKGPGQSRRLCLFLSFLVAGATTFLCLHFGVIGPQREEPK----- 65
Qy 62 DSYWDPNDEESMNSPCWQVKQLRVKMLRTSEETISTVQEQQNISPLVRERGPR 121
Dh 66 ----DP-----SLISPLQA-----VRSSRTPS-----DK 87
Qy 122 VAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVTHEKGF 181
Dh 88 PVAHVVA-----NPQAEGL--QWLSGRANALLANGVELRDNLQVVPSEGL 131
Qy 182 YIIYSQTYFRFOERIKENTKNDKQWQVIYKYT-----SYDDPILLMKSARNSCWSK-- 233
Dh 132 YLIYSQVLFKQ-----GCPSTHVLLTHTSRIASVSYQTKVNLLSAISKPCQRETP 182
Qy 234 --DAEYGLYIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS--FFG 276
Dh 183 EGAERKPYEPIYLGGVFQLEKDRLSAEINLPDYLDFAESGQVYFG 229
RESULT 11
JQ1344
tumor necrosis factor alpha precursor - horse
N:Alternate names: cachectin; TNF alpha
C:Species: Equus caballus (domestic horse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JQ1344
R:Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f
A:Reference number: JQ1344; MUID:92084125; PMID:1748301
A:Accession: JQ1344
A:Molecule type: DNA
A:Residues: 1-234 <SUX>
A:Cross-references: UNIPROT:P29553; GB:M64087; NID:G164244; PIDN:AAA30959.1; PID:G164245
C:Comment: This protein is an important proximal mediator of endotoxemia.
C:Genetics:
A:Gene: TNF-alpha
A:Introns: 62/3; 79/1; 95/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cycotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
```

```
F:19/20/Binding site: myristate (Lys) (covalent) #status predicted
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:146-178/Disulfide bonds: #status predicted
```

```
Query Match 8.9%; Score 131; DB 1; Length 234;
Best Local Similarity 20.8%; Pred. No. 0.0012;
Matches 60; Conservative 40; Mismatches 89; Indels 100; Gaps 13;
```

```
Qy 8 GGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFL-----K 59
Dh 22 GPGQSRRLCLSLFSL--VAGATTFL-----CLLHFGVIGPQR 60
```

```
Qy 60 EDDSYWDPNDEESMNSPCWQVKQLRVKMLRTSEETISTVQEQQNISPLVRERGPR 119
Dh 61 EEQL-----PNAFQSIIN-PLAQT-----LRSSRTPS----- 86
```

```
Qy 120 QVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVTHEK 179
Dh 87 DKPVAHVVA-----NPQAEGL--QWLSGRANALLANGVELRDNLQVVPFLD 130
```

```
Qy 180 GFYIYSQTYFRFOERIKENTKNDKQWQVIYKYT-----SYDDPILLMKSARNSCWSK 233
Dh 131 GLYLIYSQVLFKQ-----GCPSTHVLLTHTSRIASVSYQTKVNLLSAISKPCHE 181
```

```
Qy 234 DAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS--FFG 276
Dh 182 SPEQAEKPYEPIYLGGVFQLEKDRLSAEINQPNYLDFAESGQVYFG 230
```

## RESULT 12

S24642

tumor necrosis factor alpha precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C:Accession: I46047; S24642

R:Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tun

A:Reference number: I46046; MUID:94083525; PMID:8260599

A:Accession: I46047

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-233 &lt;CL2&gt;

A:Cross-references: UNIPROT:Q06599; EMBL:Z14137; NID:G796; PIDN:CAA78511.1; PID:G798

C:Genetics:

A:Gene: TNFA

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

```
Query Match 8.8%; Score 130.5; DB 1; Length 233;
Best Local Similarity 20.3%; Pred. No. 0.0013;
Matches 59; Conservative 43; Mismatches 95; Indels 93; Gaps 13;
```

```
Qy 3 MMEVQGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFL----- 58
Dh 17 LSEKAGGPGQSRRLCLSLFSL--VAGATTFL-----CLLHFGV 55
```

```
Qy 59 ---KEDSYWDPNDEESMNSPCWQVKQLRVKMLRTSEETISTVQEQQNISPLVR 115
Dh 56 IGPOREESPGGP---SINSPLVQT-----LRSSSQASS----- 85
```

```
Qy 116 ERGQPVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELV 175
Dh 86 ----NKPVAHVVA-----DINSPQLR-----WDSYANALMANGVKLEDNQLV 125
```

```
Qy 176 IHEKGFYIYSQTYFRFOERIKENTKNDKQWQVIYK--YTSYDDPILLMKSARNSC--- 230
Dh 126 VPADGLYLIYSQVLFKQ-----GCPSTPLFTHTSRIASVSYQTKVNLLSAISKPCHE 180
```



A; Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764  
A; Experimental source: U-937 cells  
R; Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.  
Eur. J. Biochem. 235, 431-437, 1996  
A; Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.  
A; Reference number: S62610; MUID:56202967; PMID:8631363  
A; Accession: S62610  
A; Molecule type: protein  
A; Residues: 77-99 <DAK>  
R; D'Alfonso, S.; Richiardi, P.M.  
Immunogenetics 39, 150-154, 1994  
A; Title: A polymorphic variation in a putative regulation box of the TNFA promoter region  
A; Reference number: I54522; MUID:54102809; PMID:7903959  
A; Accession: I54522  
A; Status: preliminary; translated from GB/EMBL/DBJ  
A; Molecule type: DNA  
A; Residues: 1-8 <DAL>  
A; Cross-references: GB:S68530; NID:g544751  
R; Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.  
J. Exp. Med. 176, 1053-1062, 1992  
A; Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysine  
A; Reference number: A59163; MUID:93018820; PMID:1402651  
A; Contents: annotation; identification of myristylated lysines  
R; Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bring  
J. Biol. Chem. 260, 2345-2354, 1985  
A; Title: Human tumor necrosis factor. Production, purification, and characterization.  
A; Reference number: A92511; MUID:85110974; PMID:3871770  
A; Contents: annotation; disulfide bond  
C; Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction  
out detriment to normal cells. It can also act synergistically with interferon gamma to  
C; Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely  
it are produced by different cell types and have different induction kinetics.  
C; Geneticks:  
A; Gene: GDB:TNF; TNFA  
A; Cross-references: GDB:120441; OMIM:191160  
A; Map position: 6p21.3-6p21.3  
A; Introns: 62/3; 78/1; 94/1  
C; Complex: homotrimer  
C; Superfamily: tumor necrosis factor  
C; Keywords: cytokine; cytotoxic; glycoprotein; homotrimer; lipoprotein; lymphokine; macrophage  
F; 1-76/Domain: propeptide \$status predicted <PRO>  
F; 19,20/Binding site: myristate (lys) (covalent) \$status experimental  
F; 81/Binding site: carbohydrate (Ser) (covalent) (partial) \$status experimental  
F; 145-177/Disulfide bonds: \$status experimental

Query Match	8.5%;	Score	125.5;	DB 1;	Length	233;			
Best Local Similarity	17.8%;	Pred. No.	0.0036;						
Matches	51;	Conservative	52;	Mismatches	99;	Indels	85;	Gaps	9;

  

Qy	2	AMMEVQGSPSLGQTCVLIVFTVLLQSLCAVTVVYFTNELKQMDKYKSGIAFLKED	61						
	:		:	:	:	:	:	:	:
Db	16	ALPKKTGGPGOSRRCLFLSLFSLIVAGATTFLCLLHFGVIGPQREBPFR	65						
Qy	62	DSYWDPNDESMSPCQVQWQLRQLVRKMLIRTSSETISTVQEQQNISPLVRERGQR	121						
	:		:	:	:	:	:	:	:
Db	66	-----DLSLISPLAQ-----VRSSRTPS-----DK	87						
Qy	122	VAAHITGRGRSNTLSSPNSKVEKALGRKINSWESSRSGHSFLGNLHLRNGELVTHEKGF	181						
	:		:	:	:	:	:	:	:
Db	88	PVAHVVA-----NPOREGQL--QWLNRRANALLANGVELRDQLVVPSEGL	131						
Qy	182	YYIYSQTYFRFQEBEIKENTKNDKQMVQIYKYT-----SYPDILLMKMSARNCSWK--	233						
	:		:	:	:	:	:	:	:
Db	132	YLIYSQVLFGQ-----GCPSTHVLLTHTISRTAVSYQTKVNLLSAIKSPCQRETP	182						
Qy	234	---DAEYGLYSIYOGGFIPELKENDRIFVSVTNEHLIMDHEAS--FFG	276						
	:		:	:	:	:	:	:	:
Db	183	EGEAKEKWYPIYLGGVFQLEKGRDGLSAEINRPDYLDFAESGQVYVF	229						
	:		:	:	:	:	:	:	:

Search completed: June 3, 2005, 06:25:41  
Job time : 42 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 06:07:44 ; Search time 176 Seconds  
(without alignments)  
817.581 Million cell updates/sec

Title: US-10-662-431-2

Perfect score: 1478

Sequence: 1 MAMMEVGGSGLGQTCVLIV.....NEHLIDMDHRSFPGAFVNG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	1 TN10_HUMAN	P50591 homo sapien
2	963	65.2	287	2 Q8K3G0	Q8K390 rattus norv
3	930	62.9	291	1 TN10_MOUSE	P50592 mus musculus
4	809.5	54.8	304	2 Q7T1F2	Q7T1F2 gallus gall
5	577.5	39.1	299	2 Q6DHG9	Q6DHG9 brachydanio
6	334.5	22.6	317	2 Q7ZYX9	Q7ZYX9 brachydanio
7	307.5	20.8	287	2 Q90WT9	Q90WT9 gallus gall
8	305.5	20.7	214	2 Q9DDZ5	Q9DDZ5 brachydanio
9	291	19.7	63	2 Q6JSD9	Q6JSD9 homo sapien
10	267.5	18.1	318	1 TN11_RAT	Q9ESE2 r tumor nec
11	258.5	17.5	316	1 TN11_MOUSE	Q35235 h tumor nec
12	251.5	17.0	317	1 TN11_HUMAN	O14788 h tumor nec
13	189.5	12.8	279	1 TNF6_MOUSE	P41047 mus musculus
14	187	12.7	280	1 TNF6_CERTO	Q9BDN1 cercocobus
15	186	12.6	281	1 TNF6_HUMAN	P48023 homo sapien
16	185	12.5	280	1 TNF6_MACFA	P63308 macaca fasc
17	185	12.5	280	1 TNF6_MACMU	P63307 macaca mula
18	185	12.5	280	1 TNF6_MACNE	P63306 macaca neme
19	184.5	12.5	279	2 Q7TMV9	Q7TMV9 mus musculus
20	184	12.4	272	1 TNF5_CHICK	Q918D8 gallus gall
21	182	12.3	282	1 TNF6_PIG	Q9BEA8 sus scrofa
22	180	12.2	252	2 Q8K3Y8	Q8K3Y8 mus musculus
23	178.5	12.1	280	2 Q861W5	Q861W5 felis silve
24	177.5	12.0	278	1 TNF6_RAT	P36940 rattus norv
25	175.5	11.9	169	2 Q9WY90	Q9WY90 marmota mon
26	175	11.8	252	2 Q80Y20	Q80Y20 mus musculus
27	173	11.7	252	2 Q8K3Y7	Q8K3Y7 rattus norv
28	166	11.2	251	2 Q8NFE9	Q8NFE9 homo sapien
29	164	11.1	261	1 TNF5_BOVIN	P51749 bos taurus
30	163.5	11.1	131	2 Q6J3G6	Q6J3G6 canis famil
31	160	10.8	174	1 TN15_HUMAN	O95150 homo sapien

32	159.5	10.8	240	1 TN14_HUMAN	O43557 homo sapien
33	157	10.6	154	2 Q8MJ19	Q8MJ19 macaca mula
34	153.5	10.4	227	2 Q7T2Q3	Q7T2Q3 cyprinus ca
35	152.5	10.3	239	1 TN14_MOUSE	Q9QYH9 mus musculus
36	152	10.3	261	1 TNF5_CALJA	Q9BDN3 callithrix
37	150.5	10.2	261	1 TNF5_AOTTR	Q9BDM3 aotus trivi
38	149.5	10.1	260	1 TNF5_FELCA	Q97605 felis silve
39	149	10.1	241	2 Q6U817	Q6U817 lateolabrax
40	148	10.0	261	1 TNF5_CERTO	P63305 cercocobus
41	148	10.0	261	1 TNF5_MACMU	P63304 macaca mula
42	147.5	10.0	260	1 TNF5_CANFA	O97626 canis famil
43	147.5	10.0	261	1 TNF5_HUMAN	P29965 homo sapien
44	144.5	9.8	216	2 Q70332	O70332 mesocricetu
45	143	9.7	261	1 TNF5_PIG	Q95mq5 sus scrofa

## ALIGNMENTS

RESULT 1

ID TN10\_HUMAN STANDARD; PRT; 281 AA.  
AC P50591;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TNFAL1 protein) (Apo-2 ligand) (Apo-2L).  
GN Name=TNFSF10; Synonyms=APO2L, TRAIL;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;  
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,  
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,  
RA Goodwin R.G.;  
RT "Identification and characterization of a new member of the TNF family that induces apoptosis.";  
RL Immunity 3:673-682(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96278649; PubMed=8663110; DOI=10.1074/jbc.271.22.12687;  
RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,  
RA Ashkenazi A.;  
RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor necrosis factor cytokine family.";  
RL J. Biol. Chem. 271:12687-12690(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[4]  
X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.  
MEDLINE=20017054; PubMed=1054288; DOI=10.1016/S097-2765(00)80207-5;  
Hymowitz S.G., Christinger H.W., Fuh G., Uitsch M., O'Connell M.,  
Kelley R.F., Ashkenazi A., de Vos A.M.;  
"Triggering cell death: the crystal structure of Apo2L/TRAIL in a  
complex with death receptor 5";  
Mol. Cell 4:563-571 (1999).  
[5]  
X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.  
PubMed=10542098; DOI=10.1038/14935;  
Mongkolkeha J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
Jones E.Y., Screaton G.R.;  
"Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
specificity in apoptotic initiation";  
Nat. Struct. Biol. 6:1048-1053 (1999).  
[6]  
X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.  
MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;  
Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin H.C.,  
Sung Y.C., Oh B.-H.;  
"2.8 A resolution crystal structure of human TRAIL, a cytokine with  
selective antitumor activity";  
Immunity 11:253-261 (1999).  
-1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,  
TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and  
possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity  
may be modulated by binding to the decoy receptors  
TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot  
induce apoptosis.  
-1- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per  
trimer.  
-1- SUBUNIT: Homotrimer.  
-1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
-1- TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung  
and prostate.  
-1- SIMILARITY: Belongs to the tumor necrosis factor family.  
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-----  
EMBL; U37518; AAC50332.1; -;  
EMBL; U57059; AAB01233.1; -;  
EMBL; BC032722; AAB32722.1; -;  
PDB; 1D0G; X-ray; A/B/D=114-281.  
PDB; 1D2Q; X-ray; A=114-281.  
PDB; 1D4V; X-ray; B=119-281.  
PDB; 1DG6; X-ray; A=91-281.  
PDB; 1DU3; X-ray; D/E/F/J/K/L=114-281.  
Genew; HGNC:11925; TNFSF10.  
H-InvDB; HIX0003863; -;  
MM; 603598; -;  
GO; GO:0005887; C: integral to plasma membrane; TAS.  
GO; GO:0005625; C: soluble fraction; TAS.  
GO; GO:0005102; F: receptor binding; TAS.  
GO; GO:0007267; P: cell-cell signaling; TAS.  
GO; GO:0006917; P: induction of apoptosis; TAS.  
GO; GO:0043123; P: positive regulation of apoptosis; TAS.  
GO; GO:0007165; P: signal transduction; TAS.  
InterPro; IPR006052; TNF family.  
InterPro; IPR008983; TNF like.  
Pfam; PF00229; TNF; 1.  
ProDom; PD002012; TNF\_subf; 1.  
SMART; SM00207; TNF; 1.  
PROSITE; PS00251; TNF\_1; 1.

DR PROSITE; PS50049; TNF\_2; 1.  
KW 3D-structure; Apoptosis; Cytokine; Metal-binding; Signal-anchor;  
Transmembrane; Zinc.  
FT DOMAIN 1 17 Cytoplasmic (Potential).  
FT TRANSMEM 18 38 Signal-anchor for type II membrane  
protein (Potential).  
FT METAL 39 281 Extracellular (Potential).  
FT STRAND 123 127 Zinc.  
FT STRAND 149 150  
FT STRAND 163 165  
FT STRAND 167 170  
FT TURN 171 172  
FT STRAND 173 176  
FT STRAND 180 193  
FT TURN 198 199  
FT STRAND 205 213  
FT STRAND 220 228  
FT TURN 233 234  
FT STRAND 237 250  
FT TURN 252 253  
FT STRAND 255 260  
FT HELIX 263 265  
FT STRAND 266 267  
FT TURN 270 272  
FT STRAND 274 279  
SQ SEQUENCE 281 AA; 32509 MW; DDAAAF78DAAB2P6D CRC64;  
  
Query Match 100.0%; Score 1478; DB 1; Length 281;  
Best Local Similarity 100.0%; Pred. No. 4.4e-113;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNELKQMDKYSGKIACFLKE 60  
Db 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNELKQMDKYSGKIACFLKE 60  
Qy 61 DDSYDPNDEESMNSPCQVKWLRLQVRKWLRLTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DDSYDPNDEESMNSPCQVKWLRLQVRKWLRLTSEETISTVQEKQONISPLVRERGQ 120  
Qy 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 180  
Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 180  
Qy 181 FYIYSQTYFRFOBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
Db 181 FYIYSQTYFRFOBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
  
RESULT 2  
Q8K3G0 ID Q8K3G0 PRELIMINARY; PRT; 287 AA.  
AC Q8K3G0;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DT TNF-related apoptosis inducing ligand.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OC NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DA;  
RA Mueller A.M., Giegerich G.;  
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY115578; AAM49797.1; -;  
DR HSSP; PS0591; ID2Q.  
DR GO; GO:0016020; C: membrane; IEA.



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CC	-----	
DR	ENBL; U37522; AAC52345.1; --	
DR	HSP; PS0591; ID2Q.	
DR	MGD; MGI:107414; Tnfsf10.	
DR	InterPro; IPR006052; TNF family.	
DR	InterPro; IPR008983; TNF_like.	
DR	InterPro; IPR001636; TNF_subf.	
DR	Pfam; PF00229; TNF; 1.	
DR	ProDom; PD002012; TNF_subf; 1.	
DR	SMART; SM00207; TNF; 1.	
DR	PROSITE; PS00251; TNF; 1.	
DR	PROSITE; PS00049; TNF_2; 1.	
KW	Apoptosis; Cytokine; Signal-anchor; Transmembrane.	
FT	DOMAIN 1 17 Cytoplasmic (Potential).	
FT	TRANSMEM 18 38 Signal-anchor for type II membrane protein (Potential).	
FT	DOMAIN 39 291 Extracellular (Potential).	
FT	CARBOHYD 52 52 N-linked (GlcNAc...) (Potential).	
SQ	SEQUENCE 291 AA; 33477 MW; 3PEACAB9FD7D802 CRC64;	
Query Match 62.9%; Score 930; DB 1; Length 291;		
Best Local Similarity 65.6%; Pred. No. 4.4e-68;		
Matches 177; Conservative 37; Mismatches 50; Indels 6; Gaps 1;		
QY	17 VLIVITVLLOSICVAVTYVYFNELKOMQDKYKSGIACFLKEDDSYWPDEESMNSP 76	
DB	21 ICIVLQLVLQAVSVAVTYVYFNEMKQLQDNYSKIGLACFSTKDFDWDSTDGEILNRP 80	
QY	77 CMOVKQMLROLVKMTILRTSEETISTVQEKQNI SPLVRGRFORVAAHITGTRGSNTL 136	
DB	81 CLQVKQLQLIEVTLRTFQDTSIVPEQLSTPLPRGGRQKVAHITGTRNSA 140	
QY	137 SSPNSKNEKALGRKINSWESSRSGHGSFLSNLHLNCELVIHEKGFYIYYSQTYPRFOEE- 195	
DB	141 LIPISKDGTIGQKIESWESSRKGHGSFLNHLPRNGELVIEQGLYIYYSQTYPRFOEAE 200	
QY	196 -----IKENTYNDKQMVQIYKYKTSYDPDPTLLMKSAKNSCWDKAEVGLSIYQGGIFEL 250	
DB	201 DASKMVSQKVRVTKQLVQVYIYKYKTSYDPDPTVLVLMKSAKNSCWDKAEVGLSIYQGGIFEL 260	
QY	251 KENDRIFSVVTNHLMDMDEAHSFFGAFLV 280	
DB	261 KENDRIFSVVTNHLMDLQDEASFFGAFLI 290	
RESULT 4		
ID	Q7T1F2 PRELIMINARY; PRT; 304 AA.	
AC	Q7T1F2; PRELIMINARY; 25, Created	
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Tumor necrosis factor related apoptosis inducing ligand.	
GN	Names=TRAIL;	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
OC	Gallus.	
OX	NCBI_TaxID=9031;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Spleen;	
RA	Saved A.A.; Horiuchi H., Furusawa S., Matsuda H.;	
RT	"Molecular Cloning and Characterization of Chicken Tumor Necrosis	
RT	Factor (TNF)-Superfamily Ligands, CD30L and TNF-Related Apoptosis	
RT	Inducing Ligand (TRAIL).";	
RL	J. Vet. Med. Sci. 66:643-650 (2004).	
DR	ENBL; AB114678; BAC79267.1; --	



RA	Bridgham J.T., Johnson A.L.;
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY057941; AAL23702.1; -;
DR	HSSP; P50591; 1D2Q.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR	GO; GO:0006955; P:immune response; IEA.
DR	Pfam; PF00229; TNF; 1.
DR	PRINTS; PR01234; TNECROSISFCT.
DR	ProDom; PD002012; TNF_subf. 1.
DR	SMART; SM00207; TNF; 1.
DR	PROSITE; PS50049; TNF_2; 1.
SQ	SEQUENCE 287 AA; 32092 MW; D806ELC95087B108 CRC64;
Query Match 20.8%; Score 307.5; DB 2; Length 287;	
Best Local Similarity 32.3%; Pred. No. 5.3e-17;	
Matches 93; Conservative 46; Mismatches 110; Indels 39; Gaps 11	
Qy	18 LIVIFTVLLQ--SLCVAVTYVYFT-----NELKQM--QKYKSGGIACFLKEDDSYWD 666
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd	8 LLHAFSLQLPLICTAPEWAGTWSQALQNAPFLRKAQSQGSSELRCLQLINQQDEG 67
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Qy	67 PNDESMMNSPCQWKQQLRVLRKMILRTSEETI--STVOEKQ--NISP-LVYREGP 119
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd	68 SNLEELISNOSC----LKLANTIKAYVATVTNISRSVNVEAQSKSYFNISEGVATKTL 123
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Qy	120 QRVAAHIT-----TGTRGRNTLSGNPKNEKALKGRKINSWESSRSSGHSLSNLHLR 170
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd	124 GKPSAHLIFRPONPAQDGSSRRFGNLS-----QSCRHAITRWEDS-TIHSLQNITYR 175
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Qy	171 NGELIVIHKEGFYYIYSOTYFRPFBEIKENTKNDKMQVQIYKYTSYPDPILLMKSRNSC 230
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd	176 DGLRLVNAQGKYYVYSQIYFRYSRDGAGARVSVPOLVCINWKTYSQPILLKKGVGTCK 235
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Qy	231 WSKDAEYGLSVSIYGGIFELKENDRIFVSVTNEHLIDMDHEASPGAF 278
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd	236 WAPEAEYGLHALYQGGLFELKAGDELFSVSSLAIDYSDDAAASYPGAF 283
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
RESULT 8	
Q9DDZ5	PRELIMINARY; PRT; 214 AA.
ID	Q9DDZ5 PRELIMINARY; PRT; 214 AA.
AC	Q9DDZ5; 01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	TRAIL-like protein.
GN	Name=tnfsf101;
OS	Brachydanio rerio (zebrafish) (Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; Danio.
OX	NBI_TaxID=7955;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Bohe J., Goetz F.W.;
RT	"Molecular cloning and expression of a TNF receptor and two TNF ligands in the fish ovary."
RL	Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
DR	EMBL; AF250041; AAG47640.1; -;
DR	HSSP; P50591; 1D2Q.
DR	ZFIN; ZDB-GENE-010801-1; tnfsf101.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR	GO; GO:0006955; P:immune response; IEA.
DR	InterPro; IPR006052; TNF_family.
DR	InterPro; IPR008983; TNF_like.
DR	Pfam; PF00229; TNF; 1.
DR	ProDom; PD002012; TNF_subf. 1.
DR	SMART; SM00207; TNF; 1.
DR	PROSITE; PS50049; TNF_2; 1.
SQ	SEQUENCE 214 AA; 24093 MW; 98C00247AFF691AA CRC64;

Query Match 20.7%; Score 305.5; DB 2; Length 214;  
 Best Local Similarity 37.6%; Pred. No. 5.3e-17;  
 Matches 62; Conservative 37; Mismatches 59; Indels 7; Gaps 3;

QY 120 QVAAHTITGRGSRNT-----LSSPNSKNEKALGRKINSWESSRSGHSFPLNHLRNGEL 174  
 DB 47 QRPASHLTSSASDNRPSQSDMHQPDQLHQSCRPVHTW-ANKSFGAHLNMTLTNGRL 105  
 QY 175 VIHEKGFYIYSQYPRF-QEEIKENTKNDQMVOYIKYTSYDPDILLMKARSNCWSK 233  
 DB 106 RVPDQSGYIYSQYPRFSDSDQSVSHQVQCYSYKTSYLNPLQLLGKGTGKCPAP 165  
 QY 234 DAERYGLSYOQGGIFELKENDRIFFSVTVNHEILDMDEHAEFPFGAF 278  
 DB 166 DAERYGLSVYQGGIFELRAGDEVFVSPTWYVGEDSSSYFGAF 210

RESULT 9  
 Q6JSD9 PRELIMINARY; PRT; 63 AA.  
 AC Q6JSD9  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Chemokine tumor necrosis factor ligand superfamily member 10  
 DE (Fragment).  
 GN Name=TNFSF10;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung carcinoma;  
 RA Polvi A., Ruosaari S., Vendelin J., West A., Saarikko I.,  
 RA Reinikainen A., Hollmen J., Laitinen T., Mannila H., Lahesmaa R.,  
 RA Kere J.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY312579; AAL16194.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 63 AA; 7638 MW; 8F0C7936DA5AAGE6 CRC64;

Query Match 19.7%; Score 291; DB 2; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-16;  
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TNELKQMDKYSGGIACFLKEDDSYWDPNDESMNSPCQVQWQLRQLVRK 90  
 DB 1 TNELKQMDKYSGGIACFLKEDDSYWDPNDESMNSPCQVQWQLRQLVRK 52

RESULT 10  
 TN11 RAT STANDARD; PRT; 318 AA.  
 AC Q9ESE2; Q91219;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator  
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-  
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast  
 DE differentiation factor) (ODF).  
 GN Name=TNfsf11; Synonyms=Oppl, Rankl, Trance;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Tibial bone.  
 RX MEDLINE=20540945; PubMed=11092398;  
 RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,

Zheng M.H.;  
 RT "Cloning, sequence and functional characterization of the rat  
 RT homologue of receptor activator of NF-kB ligand.";  
 RL J. Bone Miner. Res. 15:2178-2186(2000).  
 RN [2]  
 RP SEQUENCE OF 266-318 FROM N.A.  
 RC STRAIN=Fischer 344;  
 RX MEDLINE=21662371; PubMed=11804028;  
 RA Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-Savas A.,  
 RA Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,  
 RA Marks S.C. Jr.;  
 RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in  
 RT the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";  
 RL Int. J. Dev. Biol. 45:853-859(2001).  
 CC -I- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hypercalcemia of malignancy.  
 CC -I- SUBUNIT: Homotrimer (by similarity).  
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
 CC similarity).  
 CC -I- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.  
 CC -I- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@sib-sib.ch).  
 CC -----  
 DR EMBL; AF187319; AAG17031.1; -.  
 DR EMBL; AF425669; AAL23963.1; -.  
 DR HSP; O35235; IOTZ.  
 DR RGD; 620784; Tnfsl1.  
 DR InterPro; IPR006052; TNF family.  
 DR InterPro; IPR008983; TNF like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; FALSE\_NEG.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Differentiation; Glycoprotein; Receptor; Signal-anchor;  
 KW Transmembrane.  
 FT CHAIN 1 318 Tumor necrosis factor ligand superfamily  
 FT member 11, membrane form.  
 FT CHAIN 141 318 Tumor necrosis factor ligand superfamily  
 FT member 11, soluble form.  
 FT DOMAIN 1 47 Cytoplasmic (Potential).  
 FT TRANSMEM 48 68 Signal-anchor for type II membrane  
 FT protein (Potential).  
 FT DOMAIN 69 318 Extracellular (Potential).  
 FT SITE 140 141 Cleavage (By similarity).  
 FT CARBOHYD 199 199 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 264 264 N-linked (GlcNAc...) (Potential).  
 FT CONFLICT 317 317 I -> M (in Ref. 2).  
 SQ SEQUENCE 318 AA; 4887A4D706AD098F CRC64;

Query Match 18.1%; Score 267.5; DB 1; Length 318;  
 Best Local Similarity 27.3%; Pred. No. 1.2e-13;  
 Matches 82; Conservative 55; Mismatches 106; Indels 57; Gaps 11;

QY 10 PSIGQTCVLIVIFVTLLQSLCVATVYVYTNELKQMDKYSGGIACF-----LKED--- 61  
 DB 43 PAASRFMTALLGLGLGVVCSIALFLYFRAQMD--PNRISDSTRCFYRLRLRENTGL 100

Qy 62 -DSYWDPNDESMSPCQVQKWLRLQVYKMLRTSEETISTVQKQKQINISPLVRGPQ 120  
 Db 101 QDSTLESEDTALPDSRCRMQAFQ-----CAVQRELOHIV-----GPO 139  
 Qy 121 R---VAAHITGT-----RGRS-----NTLSSPNSKNEKALGRKINSWESSRSGH 161  
 Db 140 RFGVPANMEGSLWDVARGPEAPQFAHLITNAADIEGSHKVSU-----SSWHDR-GW 194  
 Qy 162 SFLGNLHLNGLVIEHGFYIYSQTYRFOEEIKENTKNDKQMVQYIYKT-SYDPPI 220  
 Db 195 AKISNMTLSNGLKLRVQDGFYLYANICFRHETSGSPADYQLQMLVWVVKTSIKIPSSH 254  
 Qy 221 LLMKSARNSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLV 280  
 Db 255 NLMKGGSTKNWGSNEFHYSYINGVGFELKLRAGEISVQVSNPSLDDPDQATYFGAFK 314

RESULT 11

TN11\_MOUSE STANDARD; PRT; 316 AA.

AC Q35235; Q35306; Q9JJK8; Q9JJK9; Q9RIY0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator  
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-  
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast  
 DE differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)  
 DE (OCIF).  
 GN Name=Tnfrsf11; Synonyms=OPGL, RANKL, Trance;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Hybridoma;  
 RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;  
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlicki J., Chao M.,  
 RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,  
 RA Choi Y.;  
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family  
 RT that activates c-Jun N-terminal kinase in T cells.";  
 RL J. Biol. Chem. 272:25190-25194(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Thymic lymphoma;  
 RX MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;  
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
 RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,  
 RA Galibert L.;  
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
 RT and dendritic-cell function.";  
 RL Nature 390:175-179(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;  
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,  
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,  
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,  
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,  
 RA Boyle W.J.;  
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast  
 RT differentiation and activation.";  
 RL Cell 93:165-176(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Bone marrow stroma;  
 RX MEDLINE=98188248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;  
 RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M.,  
 RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,

RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;  
 RT "Osteoclast differentiation factor is a ligand for  
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical  
 RL to TRANCE/RANKL.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=129;  
 RX MEDLINE=992114075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;  
 RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,  
 RA Ueda M., Higashio K.;  
 RT "Cloning and characterization of the gene encoding mouse osteoclast  
 RT differentiation factor.";  
 RL Gene 230:121-127(1999).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;  
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;  
 RT "Determination of three isoforms of the receptor activator of nuclear  
 RT factor-kappaB ligand and their differential expression in bone and  
 RT thymus.";  
 RL Endocrinology 142:1419-1426(2001).  
 RN [7]  
 RP SEQUENCE OF 139-147. PROCESSING, AND N-GLYCOSYLATION.  
 RX MEDLINE=98240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;  
 RA Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,  
 RA Schloendorff J., Tempst P., Choi Y., Blobel C.P.;  
 RT "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-  
 RT converting enzyme-like protease in shedding of TRANCE, a TNF family  
 RT member involved in osteoclastogenesis and dendritic cell survival.";  
 RL J. Biol. Chem. 274:13613-13618(1999).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.  
 RX MEDLINE=21464816; PubMed=11581298;  
 RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;  
 RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants  
 RT of receptor-ligand specificity.";  
 RL J. Clin. Invest. 108:971-979(2001).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.  
 RX MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M106525200;  
 RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;  
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at  
 RT 2.2-A resolution.";  
 RL J. Biol. Chem. 277:6631-6636(2002).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hypercalcemia of malignancy.  
 CC -1- SUBUNIT: Homotrimer.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted  
 CC (isoforms 1 and 2); Cytoplasmic (isoform 3).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=035235-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=035235-2; Sequence=VSP\_006449;  
 CC Name=3;  
 CC IsoId=035235-3; Sequence=VSP\_006448;  
 CC -1- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,  
 CC but not in nonlymphoid tissues and is abundantly expressed in T  
 CC cells but not in B cells. A high level expression is also seen in  
 CC the trabecular bone and lung.  
 CC -1- PTM: N-glycosylated.  
 CC -1- PTM: The soluble form of isoform 1 derives from the membrane form  
 CC by proteolytic processing. The cleavage may be catalyzed by  
 CC ADAM17. A further shorter soluble form was observed.  
 CC -1- DISEASE: Deficiency in Tnfrsf11 results in failure to form lobulo-





RX MEDLINE=95388076; PubMed=7544870; DOI=10.1016/0161-5890(95)00016-8;  
RA Peitsch M.J., Tschopp J.J.;  
RT "Comparative molecular modelling of the Fas-ligand and other members  
RL of the TNF family.";  
RN Mol. Immunol. 32:761-772(1995).  
[3]  
RP SEQUENCE FROM N.A. (ISOFORM FASL).  
RX MEDLINE=95196085; PubMed=7889405; DOI=10.1016/1074-7613(94)90106-6;  
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,  
RN Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;  
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a TNF  
RL family gene cluster.";  
RN Immunol. 1:131-136(1994).  
[4]  
RP SEQUENCE FROM N.A. (ISOFORM FASL).  
RX STRAIN=BALB/c;  
RA Femer M.H., Shioda T., Isebacher K.J.;  
RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in two  
RL amino acids";  
RN Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
[5]  
RP SEQUENCE FROM N.A. (ISOFORM FASL).  
RX STRAIN=C3H; Tissue=Spleen;  
RA Aytoldi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,  
RN Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;  
RT "Cloning and expression of a short Fas ligand: a new alternatively  
RL spliced product of the mouse Fas ligand gene.";  
RN Blood 94:3456-3467(1999).  
[6]  
RP CHARACTERIZATION OF VARIANT GLD.  
RX MEDLINE=96091792; PubMed=7495745;  
RA Hahne M., Peitsch M.C., Immler M., Schroeter M., Lowin B.,  
RN Rousseau M., Bron C., Renno T., French L., Tschopp J.;  
RT "Characterization of the non-functional Fas ligand of gld mice.";  
RN Int. Immunol. 7:1381-1386(1995).  
[7]  
RP VARIANTS ALA-184 AND GLY-218.  
RX STRAIN=BALB/c, C3H, C57BL/6, DBA/1, DBA/2, MRL, NOD, NZB, NZW, and  
RN SJL;  
RX MEDLINE=97268671; PubMed=9108079; DOI=10.1073/pnas.94.8.3914;  
RA Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,  
RN Yagita H.;  
RT "Polymorphism of murine Fas ligand that affects the biological  
RL activity";  
RN Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).  
CC -i- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
CC transduces the apoptotic signal into cells. May be involved in  
CC cytotoxic T cell mediated apoptosis and in T cell development.  
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
CC peripheral tolerance, in the antigen-stimulated suicide of mature  
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
CC modulates its effects (By similarity).  
CC -i- SUBUNIT: Homotrimer (Probable).  
CC -i- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);  
CC Secreted (isoforms FASL and FASLS).  
CC -i- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=FasL;  
CC IsoId=P41047-1; Sequence=Displayed;  
CC Name=FasLS;  
CC IsoId=P41047-2; Sequence=VSP\_006445;  
CC -i- PM: The soluble form derives from the membrane form by  
CC proteolytic processing (By similarity).  
CC -i- DISEASE: A deficiency in this protein is the cause of generalized  
CC lymphoproliferation disease phenotype (gld). Gld mice present  
CC lymphadenopathy and autoantibody production. The phenotype is  
CC recessively inherited.  
CC -i- SIMILARITY: Belongs to the tumor necrosis factor family.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U06948; AAA17800.1; -;  
DR EMBL; U10984; AAA19778.1; -;  
DR EMBL; S76752; AAB33780.1; -;  
DR EMBL; U58995; AAB02915.1; -;  
DR EMBL; AF119335; AAD52106.1; -;  
DR PIR; A53062; A53062.  
DR HSP; P50591; IDG6.  
DR MGD; MGI:99255; Tnfaf6.  
DR InterPro; IPR008064; Fas\_ligand.  
DR InterPro; IPR006053; TNF\_abc.  
DR InterPro; IPR006052; TNF\_family.  
DR InterPro; IPR008983; TNF\_like.  
DR InterPro; IPR003636; TNF\_subf.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01681; FASLIGAND.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
DR Alternative splicing; Apoptosis; Cytokine; Disease mutation;  
KW Glycoprotein; Polymorphism; Signal-anchor; Transmembrane.  
FT Tumor necrosis factor ligand superfamily  
FT CHAIN 1 279  
FT  
FT CHAIN 128 279  
FT Tumor necrosis factor ligand superfamily  
FT member 6, soluble form (By similarity).  
FT Cytoplasmic (Potential).  
FT Signal-anchor for type II membrane  
FT protein (Potential).  
FT Extracellular (Potential).  
FT Pro-rich.  
FT Poly-Pro. (By similarity).  
FT Cleavage (By similarity).  
FT POTENTIAL.  
FT N-linked (GLNAC. .) (Potential).  
FT CARBOHYD 117 117  
FT N-linked (GLNAC. .) (Potential).  
FT CARBOHYD 182 182  
FT N-linked (GLNAC. .) (Potential).  
FT CARBOHYD 248 248  
FT N-linked (GLNAC. .) (Potential).  
FT CARBOHYD 258 258  
FT Missing (in isoform FASLS).  
FT VARSPLIC 1 210  
FT  
FT VARIANT 184 184  
FT T -> A (in strain BALB/c, strain DBA/1  
FT and strain DBA/2; enhances cytotoxicity).  
FT E -> G (in strain BALB/c, strain DBA/1  
FT and strain DBA/2; enhances cytotoxicity).  
FT F -> L (in gld; abolishes binding of FASL  
FT to its receptor).  
FT SQ SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;  
Query Match 12.8%; Score 189.5; DB 1; Length 279;  
Best Local Similarity 25.8%; Pred. No. 2.5e-07;  
Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;  
QY 83 QLRQLVKRMLRTSEETITVQEKQNI SPLVRGPRVAAHITGRGRSNTLSSNSK 142  
DB 111 ELREFTNQSL-----KVSSFQKIANPSTPSKKEPSV-AHLTG-----NPHSR 154  
QY 143 NEKALGRKINSWSSRSGHSLNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKN 202  
DB 155 SIPL-----EWEDT-YGTALISGVKKYKGLVINETGLYFVYSKVYFRGQ-----SCN 201  
QY 203 DKQWQYIY-KYTSYDPDILLMKASR-NSCWKDAEYGLSYICGGIFELKENDRIFVSV 260  
DB 202 NQPLNHKVMRNKSKYPEDLVMEKRLNYCTT--GQIWAHSSYLGAVFNLTSADHLVNI 259  
QY 261 TNEHLTMDMDEASFFGAF 278  
DB 260 SQLSLINFESKTFFGLY 277



RESULT 14
TNF6_CERTO
ID TNF6 CERTO STANDARD; PRT; 280 AA.
AC Q9BDN1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand) (CD95L protein).
DE GN Name=TNFSF6; Synonyms=CD95L, FASL;
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopithecinae; Cercocebus.
NCBI_TaxID=9531;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Lymphocytes;
RC MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
CC -I- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3 modulates its effects (By similarity).
CC -I- SUBUNIT: Homotrimer (Probable).
CC -I- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity).
CC -I- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.
-----
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-----
DR EMBL; AF344847; AAC37606.1; --
DR HSPG; PS0591; I02Q.
DR InterPro; IPRO08064; Fas_ligand.
DR InterPro; IPRO06053; TNF_abc.
DR InterPro; IPRO06052; TNF_family.
DR InterPro; IPRO08983; TNF_like.
DR InterPro; IPRO03636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
FT FT CHAIN 1 280 FT   member 6, membrane form FT   Tumor necrosis factor ligand superfamily member 6, soluble form (By similarity).
FT FT TRANSMEM 81 101 FT   Cytoplasmic (Potential) FT   Signal-anchor for type II membrane protein (Potential).
FT FT DOMAIN 102 280 FT   Extracellular (Potential).
FT FT DOMAIN 4 69 FT   Pro-rich. FT FT DOMAIN 45 64 FT   Poly-Pro. FT FT SITE 128 129 FT   Cleavage (By similarity).
FT FT DISULPID 201 232 FT   Potential.



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SQ SEQUENCE 281 AA; 31485 MW; ABA6EB358246E9BB CRC64;
Query Match 12.6%; Score 186; DB 1; Length 281;
Best Local Similarity 22.1%; Pred. NO. 4.9e-07;
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;
Qy 4 MEVOGGSLSGTCVLIVIFTVLQSLCVAV---TVVYFTNELKQMDKYKSGIACFLKE 60
Db 71 LKKGNHSTG-LCLLVWFVFLVALVGLGWMFQLFHLOKELAEURESTQMHNTASSLEK 129
Qy 61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 130 QIGHPSPEPE-----KKELRKV----- 146
Qy 121 RVAAHITGTRGRSNVTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
Db 147 ---AHLT---GKSNRSRMP-----LEWEDT-YGIVLLSGVKYKKGGLVINETG 187
Qy 181 FYIYQTYFRFOBEIKENTKNDKMQVQYIY-KYTSYDPDPILLMKSARN-----CWSK 233
Db 188 LYFYISKYIFRGQ-----SCNNLPLSHKVYRNRSKYFQDLVMMEGKRMMSYCTTGQMMWAR 241
Qy 234 DAEXGLYSYOGGIFELKENDRIFVSVTNEHLIDMDHEASPFQAF 278
Db 242 -----SSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFEGLY 279
```

Search completed: June 3, 2005, 06:24:55  
Job time : 178 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 11:54:33 ; Search time 162 Seconds  
(without alignments)  
670.862 Million cell updates/sec

Title: US-10-662-431-2

Perfect score: 1478

Sequence: 1 MAMMEVQSGPSLQGTCLIV.....NEHLIDMDHEASFGAPLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 55

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 500 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	2	AAW19777 Novel cyt
2	1478	100.0	281	2	AAW27134 Human Apo
3	1478	100.0	281	2	AAW19787 Human apo
4	1478	100.0	281	2	AAW76829 Human TL2
5	1478	100.0	281	2	AAW56760 Human TRA
6	1478	100.0	281	2	AAW44354 Human AGP
7	1478	100.0	281	2	AAW01517 Protein a
8	1478	100.0	281	2	AAW27012 Human Apo
9	1478	100.0	281	3	AAW81956 Human Apo
10	1478	100.0	281	3	AAW24038 Human PRO
11	1478	100.0	281	3	AAW08545 Amino aci
12	1478	100.0	281	3	AAW28691 Human AGP
13	1478	100.0	281	4	AAW50977 Human PRO
14	1478	100.0	281	4	AAW67243 Human Apo
15	1478	100.0	281	4	AAW11031 Human TNF
16	1478	100.0	281	4	AAW48350 Human TL2
17	1478	100.0	281	5	AAW08133 Human TRA
18	1478	100.0	281	5	AAW31630 Human TRA
19	1478	100.0	281	5	AAW75062 Human TNF
20	1478	100.0	281	5	AAW51077 Human TNF
21	1478	100.0	281	5	AAW51954 Human Apo
22	1478	100.0	281	5	AAW19095 C neoform
23	1478	100.0	281	5	AAW79593 Human TNF
24	1478	100.0	281	6	ABG73861 Human Apo
25	1478	100.0	281	6	ABU10205 Human Apo

26	1478	100.0	281	6	ABU71443 Human neo
27	1478	100.0	281	6	ABG72738 Human TNF
28	1478	100.0	281	6	AAO29543 Human TRA
29	1478	100.0	281	6	ABU08558 Human TNF
30	1478	100.0	281	6	ABR42313 Human TRA
31	1478	100.0	281	6	ABG71905 Human TRA
32	1478	100.0	281	6	ABP60546 Human tum
33	1478	100.0	281	6	AAE36258 Human TNF
34	1478	100.0	281	6	AAO31151 Human TNF
35	1478	100.0	281	6	ABO25125 Human TNF
36	1478	100.0	281	7	ADB61471 Native hu
37	1478	100.0	281	7	ADC35202 Human TNF
38	1478	100.0	281	7	ADD14080 Human src
39	1478	100.0	281	7	ADD19010 Human dis
40	1478	100.0	281	7	ABW02276 Human TRA
41	1478	100.0	281	8	ADE76953 Human pro
42	1478	100.0	281	8	ADK72311 Human Apo
43	1478	100.0	281	8	ADK72303 Human Apo
44	1478	100.0	281	8	ADK72304 Human Apo
45	1478	100.0	281	8	ADK72296 Human wil
46	1478	100.0	281	8	ADK72310 Human Apo
47	1478	100.0	281	8	ADJ63976 Human apo
48	1478	100.0	281	8	ADL71816 Human apo
49	1478	100.0	281	8	ADK15498 Human TRA
50	1478	100.0	281	8	ADN07587 Human apo
51	1478	100.0	281	8	ADR14209 Human NF-
52	1478	100.0	281	8	ADK82215 Human TRA
53	1478	100.0	281	8	ADS88000 Tumour tr
54	1478	100.0	281	8	ABO84415 Human can
55	1478	100.0	281	8	ADP23388 PRO poly

ALIGNMENTS

RESULT 1

AAW19777  
ID AAW19777 standard; protein; 281 AA.

XX AAW19777;

XX AC AAW19777;

XX DT 22-SEP-1997 (first entry)

XX DE Novel cytokine Apo-2 ligand.

XX KW Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.

XX OS Homo sapiens.

Key	Location/Qualifiers
Peptide	1..281
Region	/note="Claim 4"
Protein	/label= Cytoplasmic_region
Region	15..281
Region	/note="Claim 3"
Protein	15..40
Region	/label= Transmembrane_region
Protein	41..281
Region	/note="Claim 2"
Region	41..281
Modified-site	/label= Extracellular_region
Protein	109
Protein	/label= Glycosylation
Protein	/note="putative N-linked glycosylation site"
Protein	114..281
Protein	/note="Claim 1"

W09725428-A1.

17-JUL-1997.

08-JAN-1997;

97WO-US0000272.

```

XX 09-JAN-1996; 96US-00584031.
PR (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX
XX WPI: 1997-372867/34.
XX N-PSDB; AAT72796.
XX
XX Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce
XX apoptosis for the treatment of breast and colon cancer.
XX
XX Claim 4; Fig 1a; 72pp; English.
XX
XX A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian
XX cell apoptosis. It is believed to be a member of the tumour necrosis
XX factor cytokine family. Its amino acid sequence was deduced from a cDNA
XX clone (AAT72796) isolated from a human placental cDNA library. Apo-2
XX ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-
XX 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells
XX transformed or transfected with a vector contg. Apo-2 ligand nucleic
XX acid. They can be used to induce apoptosis in mammals and to treat
XX pathological conditions such as cancer (esp. breast or colon cancer) or
XX to raise antibodies useful in diagnostic assays
XX
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1478; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-137;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
XX DB 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
XX
XX QY 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNISPLVRGPQ 120
XX DB 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNISPLVRGPQ 120
XX
XX QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
XX DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
XX
XX QY 181 FYYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYPPDPILLMKSRNSCKDAEYGLY 240
XX DB 181 FYYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYPPDPILLMKSRNSCKDAEYGLY 240
XX
XX QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
XX DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
XX
XX RESULT 2
XX AAW27134
XX ID AAW27134 standard; protein; 281 AA.
XX
XX AC AAW27134;
XX
XX 02-APR-1998 (first entry)
XX
XX Human Apoptosis inducing molecule-I (AIM-I).
XX
XX Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;
XX tumour necrosis factor ligand superfamily; AIM-I altered expression;
XX neoplasia inhibition; anti-inflammatory agent.
XX
XX Homo sapiens.
XX
XX WO9733899-A1.
XX
XX 18-SEP-1997.
XX

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PF 14-MAR-1996; 96WO-US003773.
XX
XX 14-MAR-1996; 96WO-US003773.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM;
XX
XX WPI: 1997-470807/43.
XX N-PSDB; AAT85210.
XX
XX New isolated apoptosis inducing molecule-I - used to develop products for
XX the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
XX versus host disease or inflammation.
XX
XX Claim 2; Fig 1; 82pp; English.
XX
XX The present sequence represents a human Apoptosis inducing molecule-I
XX (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand
XX superfamily. The products can be used in the diagnosis and treatment of
XX disorders related to under-expression, over-expression or altered
XX expression of AIM-I. AIM-I or agonists can be used for treating
XX autoimmune disorders including systemic lupus erythematosus,
XX immunoproliferative disease lymphadenopathy (IPL),
XX angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
XX diabetes, and multiple sclerosis, graft versus host disease, to inhibit
XX neoplasia such as tumour cell growth, to treat restenosis, to regulate
XX haematopoiesis in endothelial cell development, to stimulate peripheral
XX tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
XX used for treating cachexia, cerebral malaria, rheumatoid arthritis or
XX osteoporosis, for preventing graft-host rejection, and as anti-
XX inflammatory agents, for treating endotoxic shock or to prevent
XX activation of HIV
XX
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1478; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-137;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
XX DB 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
XX
XX QY 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNISPLVRGPQ 120
XX DB 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNISPLVRGPQ 120
XX
XX QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
XX DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
XX
XX QY 181 FYYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYPPDPILLMKSRNSCKDAEYGLY 240
XX DB 181 FYYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYPPDPILLMKSRNSCKDAEYGLY 240
XX
XX QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
XX DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
XX
XX RESULT 3
XX AAW19787
XX ID AAW19787 standard; protein; 281 AA.
XX
XX AC AAW19787;
XX
XX 24-SEP-1997 (first entry)
XX
XX Human apoptosis inducer cytokine TRAIL.
XX
XX Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
XX cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
XX

```

thrombotic microangioplasty; therapy.

Homo sapiens.

Key Location/Qualifiers

Domain 1..18 /label= Cytoplasmic\_domain

Domain 19..38 /label= Transmembrane\_domain

Domain 39..281 /label= Extracellular\_domain

note= "contains a receptor-binding region"

Cleavage-site 89..90 /note= "potential KEX2 protease processing site"

Modified-site 109..111 /note= "potential N-glycosylation site"

Cleavage-site 149..150 /note= "potential KEX2 protease processing site"

WO9701633-A1.

16-JAN-1997.

25-JUN-1996; 96WO-US010895.

29-JUN-1995; 95US-00496632.

01-NOV-1995; 95US-00548368.

(IMV ) IMMUNEX CORP.

Wiley SR, Goodwin RG;

WPI; 1997-118715/11.

N-PSDB; AAT72847.

TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected cells - useful for treating thrombotic microangiopathy, cancer and viral infection and for use in assays.

Claim 10; Page 43-44; 62pp; English.

Human tumour necrosis factor related apoptosis inducing ligand (TRAIL) (AAW19787) is a novel cytokine that induces apoptosis of certain target cells, including cancer cells and virally infected cells. Its amino acid sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in vector pPC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble polypeptides) can be expressed in host cells and used in the treatment of cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or to raise antibodies that may be useful for treating thrombotic microangiopathies

Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAMMEVGGPSLGTCTVLIIVFTVLLQSLCAVAVTVYFTTNELKQMDKYSKGIACFLKE 60

1 MAMMEVGGPSLGTCTVLIIVFTVLLQSLCAVAVTVYFTTNELKQMDKYSKGIACFLKE 60

61 DDSYWDNDDESNPCWQVKWQLROLVRKMLTSETISTVQEKQNTISPLVRERGQ 120

61 DDSYWDNDDESNPCWQVKWQLROLVRKMLTSETISTVQEKQNTISPLVRERGQ 120

121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180

121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180

181 FYYIYSQTFRFBQBEIKENTKNDKQVQIYKYTSYDPPILLMKARNCSWCKDAEYGLY 240

181 FYYIYSQTFRFBQBEIKENTKNDKQVQIYKYTSYDPPILLMKARNCSWCKDAEYGLY 240

241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 4

AAW76829

ID AAW76829 standard; protein; 281 AA.

XX AAW76829;

XX 25-JAN-1999 (first entry)

XX Human TL2 protein.

XX TR6; tumour necrosis factor related receptor; human; treatment; stroke; inflammation; arthritis; septicemia; autoimmune disease; restenosis; transplant rejection; infection; ischaemia; brain injury; bone disease; acute respiratory disease syndrome; acquired autoimmune disease syndrome; AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF; TL2. tumour necrosis factor-related apoptosis-inducing ligand.

XX Homo sapiens.

XX EF870827-A2.

XX 14-OCT-1998.

XX 23-DEC-1997; 97EP-00310562.

XX 14-MAR-1997; 97US-0041230P.

XX 09-MAY-1997; 97US-00853684.

XX 22-AUG-1997; 97US-00916625.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX Deen KC, Young PR;

XX WPI; 1998-5231156/45.

XX N-PSDB; AAV63096.

XX DNA encoding tumour necrosis factor receptor TR6 - and corresponding polypeptide, antibody, agonist, antagonist, etc.

XX Disclosure; Page 32-33; 34pp; English.

XX This sequence represents the human tumour necrosis factor (TNF)-related receptor, TL2 (also known as tumour necrosis factor-related apoptosis-inducing ligand, TRAIL). This protein is used in a method resulting in the isolation of the novel human TNF related receptor, TR6. TR6 polypeptides and polynucleotides can be used in the treatment of chronic and acute inflammation, arthritis, septicemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs. host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, (acquired autoimmune disease syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative disorders), atherosclerosis and Alzheimers disease

Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAMMEVGGPSLGTCTVLIIVFTVLLQSLCAVAVTVYFTTNELKQMDKYSKGIACFLKE 60

1 MAMMEVGGPSLGTCTVLIIVFTVLLQSLCAVAVTVYFTTNELKQMDKYSKGIACFLKE 60

61 DDSYWDNDDESNPCWQVKWQLROLVRKMLTSETISTVQEKQNTISPLVRERGQ 120

61 DDSYWDNDDESNPCWQVKWQLROLVRKMLTSETISTVQEKQNTISPLVRERGQ 120

121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180

Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180  
 QY 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQIYKYTSYDPDPILLMKSGARNSCWSKDAEYGLY 240  
 Db 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQIYKYTSYDPDPILLMKSGARNSCWSKDAEYGLY 240  
 QY 241 SIYQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
 Db 241 SIYQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 5  
 AAW56760  
 ID AAW56760 standard; protein; 281 AA.  
 XX  
 AC AAW56760;  
 XX  
 DT 05-AUG-1998 (first entry)  
 XX  
 DE Human TRAIL polypeptide.  
 XX  
 KW Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;  
 KW cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Domain 1..18  
 FT /note= "N-terminal cytoplasmic domain"  
 FT Region 19..38  
 FT /note= "transmembrane region"  
 FT Domain 39..281  
 FT /note= "extracellular domain"  
 XX  
 PN US5763223-A.  
 XX  
 PD 09-JUN-1998.  
 XX  
 PF 25-JUN-1996; 96US-00670354.  
 XX  
 PR 29-JUN-1995; 95US-00496632.  
 PR 01-NOV-1995; 95US-00548368.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Goodwin RG, Wiley SR;  
 XX  
 DR WPI; 1998-347322/30.  
 DR N-PSDB; AAV29518.  
 XX  
 XX DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful  
 PT for producing recombinant polypeptides for research and therapy of  
 PT leukaemia, lymphoma, melanoma and viral infections.  
 XX  
 PS Claim 1; Col 33-36; 28pp; English.  
 XX  
 CC This represents a human tumour necrosis factor related apoptosis ligand  
 CC (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce  
 CC apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful  
 CC for producing the recombinant TRAIL polypeptides, which may be useful in  
 CC studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells  
 CC (e.g. to isolate antigens for vaccine development). The polypeptides can  
 CC be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal  
 CC treatment of blood or bone-marrow), or to treat viral infections  
 XX  
 SQ Sequence 281 AA;  
 Query Match 100.0%; Score 1478; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVFTNELKQMDKYKSGIACFLKE 60

Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVFTNELKQMDKYKSGIACFLKE 60  
 QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120  
 Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120  
 QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180  
 Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180  
 QY 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQIYKYTSYDPDPILLMKSGARNSCWSKDAEYGLY 240  
 Db 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQIYKYTSYDPDPILLMKSGARNSCWSKDAEYGLY 240  
 QY 241 SIYQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
 Db 241 SIYQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 6  
 AAW44354  
 ID AAW44354 standard; protein; 281 AA.  
 XX  
 AC AAW44354;  
 XX  
 DT 28-MAY-1998 (first entry)  
 XX  
 DE Human AGP-1.  
 XX  
 KW Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;  
 KW bone resorption; haematopoietic disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9746686-A2.  
 XX  
 PD 11-DEC-1997.  
 XX  
 PF 06-JUN-1997; 97WO-US009895.  
 XX  
 PR 07-JUN-1996; 96US-00660562.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Johnson MJ, Simonet WS, Danilenko DM;  
 XX  
 DR WPI; 1998-042194/04.  
 DR N-PSDB; AAV15295.  
 XX  
 XX Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -  
 PT useful for treating inflammation, bone resorption and haematopoietic  
 PT diseases.  
 XX  
 PS Claim 7; Page 36-37; 54pp; English.  
 XX  
 CC The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis  
 CC factor (TNF)-related protein, involved in inflammation, myelopoiesis and  
 CC bone resorption. It has the same nucleic acid and amino acid (aa)  
 CC sequences as the TNF-related apoptosis-induced ligand (TRAIL) described  
 CC in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay  
 CC reagents for detecting AGP-1 expression. Nucleic acid complementary to  
 CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are  
 CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus  
 CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or  
 CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,  
 CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat  
 CC haematopoietic diseases associated with reduction in the number of bone  
 CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused  
 CC by disease, injury or exposure to myelosuppressive agents. Host cells,  
 CC transformed with expression vectors containing AGP-1 DNA, are used to  
 CC produce recombinant AGP-1



SQ Sequence 281 AA;  
 Query Match 100.0%; Score 1478; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60  
 DB 1 MAMMEVGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60  
 QY 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQNTSPLVRERGQ 120  
 DB 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQNTSPLVRERGQ 120  
 QY 121 RAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHG 180  
 DB 121 RAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHG 180  
 QY 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 DB 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7  
 AAY01517  
 ID AAY01517 standard; peptide; 281 AA.  
 AC AAY01517;  
 XX  
 DT 27-MAY-1999 (first entry)  
 DE Protein associated with neurodegenerative and autoimmune diseases.  
 KW Neurodegenerative disease; autoimmune disease; inflammatory disease;  
 KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;  
 KW surface receptor; TRAIL protein.  
 OS Homo sapiens.  
 XX  
 PN PR2766713-A1.  
 XX  
 PD 05-FEB-1999.  
 XX  
 PF 04-AUG-1997; 97FR-00010176.  
 XX  
 PR 04-AUG-1997; 97FR-00010176.  
 XX  
 PA (INMR ) BIO MERIEUX.  
 XX  
 PI Rieger F, Belliveau JF, Perron H;  
 XX  
 DR WPI; 1999-156177/14.  
 XX  
 PT Use of polypeptide derived from TRAIL protein for diagnosis of  
 PT degenerative disease - autoimmunity and inflammation, also useful in  
 PT prevention or treatment, and similar use of corresponding ligand and  
 PT nucleic acid.  
 XX  
 PS Claim 2; Page 13; 21pp; French.  
 XX  
 CC The specification describes the use a polypeptide corresponding to at  
 CC least the primary sequence of part of the present sequence to produce a  
 CC diagnostic, prophylactic or therapeutic composition useful in cases of  
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can  
 CC be used in treatment of neurodegenerative disease, lupus erythematosus,  
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central  
 CC nervous system cells, antigenic and specifically recognise the surface  
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and  
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an

CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific  
 CC receptors, inhibiting formation of natural complex  
 SQ Sequence 281 AA;  
 Query Match 100.0%; Score 1478; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60  
 DB 1 MAMMEVGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60  
 QY 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQNTSPLVRERGQ 120  
 DB 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQNTSPLVRERGQ 120  
 QY 121 RAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHG 180  
 DB 121 RAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHG 180  
 QY 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 DB 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8  
 AAY27012  
 ID AAY27012 standard; protein; 281 AA.  
 AC AAY27012;  
 XX  
 DT 24-SEP-1999 (first entry)  
 DE Human Apo-2 ligand (Apo-2L) polypeptide.  
 KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;  
 KW lupus; immune-mediated glomerular nephritis; human.  
 OS Homo sapiens.  
 XX  
 PN WO9936535-A1.  
 XX  
 PD 22-JUL-1999.  
 XX  
 PF 15-JAN-1999; 99WO-US001039.  
 XX  
 PR 15-JAN-1998; 98US-00007886.  
 XX  
 PR 15-APR-1998; 98US-00060533.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;  
 XX  
 DR WPI; 1999-444397/37.  
 DR N-PSDB; AAX86987.  
 XX  
 PT A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis  
 PT in mammalian cancer cells.  
 XX  
 PS Claim 1; Fig 1A; 86pp; English.  
 XX  
 CC This sequence represents a novel human cytokine, designated Apo-2 ligand  
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant  
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer  
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to  
 CC induce apoptosis for pathological conditions characterized by decreased  
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-  
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid

CC coding sequence can also be used in quantitative and screening diagnostic  
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases  
 CC associated with increased apoptosis

XX Sequence 281 AA;  
 SQ Query Match 100.0%; Score 1478; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCLVIVFTVLLQSLCAVTVYVFTNKLQMDKYKSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCLVIVFTVLLQSLCAVTVYVFTNKLQMDKYKSGIACFLKE 60  
 QY 61 DDSYWDNDDESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEKQNI SPLVREGPQ 120  
 DB 61 DDSYWDNDDESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEKQNI SPLVREGPQ 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHEKG 180  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHEKG 180  
 QY 181 FYIYSQTYFRFOBEIKENTKNDKQWQVIYKYTSYDPDILLMKSGARNSCWSKDAEYGLY 240  
 DB 181 FYIYSQTYFRFOBEIKENTKNDKQWQVIYKYTSYDPDILLMKSGARNSCWSKDAEYGLY 240  
 QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
 DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 9  
 AAY81956  
 ID AAY81956 standard; protein; 281 AA.  
 AC AAY81956;  
 XX  
 DT 10-JUL-2000 (first entry)  
 XX Human Apo-2 ligand protein sequence.

DE Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;  
 KW therapy; apoptosis; cancer.  
 KW Homo sapiens.  
 OS US6046048-A.  
 PN 04-APR-2000.  
 PD 08-JAN-1997; 97US-00780496.  
 PF 09-JAN-1996; 96US-0009755P.  
 XX (GETH ) GENENTECH INC.  
 PA Kim KJ, Ashkenazi AJ, Chuntharapai A;  
 PI WPI; 2000-282690/24.  
 XX N-PSDB; AAA07425.

DR New isolated monoclonal antibodies having antigen specificity for Apo-2  
 PT ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo  
 PT -2 ligand serum, and for treating diseases associated with increased  
 PT apoptosis.  
 PT Claim 9; Fig 1a; 46pp; English.  
 PS This sequence is the human Apo-2 ligand protein, which is recognised by  
 CC monoclonal antibodies produced by the hybridoma cell lines of the  
 CC invention. The hybridoma cell lines are deposited under the American Type  
 CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258  
 CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic

CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,  
 CC tissues, or serum. The antibodies may also be employed as therapeutics.  
 CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand  
 CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat  
 CC pathological conditions or diseases associated with increased apoptosis.  
 CC They are also useful for the affinity purification of Apo-2 ligand from  
 CC recombinant cell culture or natural sources. The Apo-2 ligand itself may  
 CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells

XX Sequence 281 AA;  
 SQ Query Match 100.0%; Score 1478; DB 3; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCLVIVFTVLLQSLCAVTVYVFTNKLQMDKYKSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCLVIVFTVLLQSLCAVTVYVFTNKLQMDKYKSGIACFLKE 60  
 QY 61 DDSYWDNDDESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEKQNI SPLVREGPQ 120  
 DB 61 DDSYWDNDDESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEKQNI SPLVREGPQ 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHEKG 180  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHEKG 180  
 QY 181 FYIYSQTYFRFOBEIKENTKNDKQWQVIYKYTSYDPDILLMKSGARNSCWSKDAEYGLY 240  
 DB 181 FYIYSQTYFRFOBEIKENTKNDKQWQVIYKYTSYDPDILLMKSGARNSCWSKDAEYGLY 240  
 QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
 DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 10  
 AAB24038  
 ID AAB24038 standard; protein; 281 AA.  
 XX  
 AC AAB24038;  
 XX  
 DT 25-JAN-2001 (first entry)  
 XX Human PRO1096 protein sequence SEQ ID NO:51.  
 DE Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;  
 KW identification; tumorigenesis; anticancer; detection.  
 KW Homo sapiens.  
 OS WO2000053750-A1.  
 PN 14-SEP-2000.  
 PD 02-DEC-1999; 99WO-US028551.  
 PF 08-MAR-1999; 99WO-US005028.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028634.  
 XX (GETH ) GENENTECH INC.  
 PA Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;  
 XX WPI; 2000-594320/56.  
 XX N-PSDB; AAC58120.  
 DR Antibodies specific for PRO polypeptides, used to diagnose and inhibit  
 PT the growth of tumors in mammals, and to identify inhibitors of PRO  
 PT polypeptide activity or expression.

XX Claim 61; Fig 36; 226pp; English.

XX The present invention describes an antibody that binds to a human protein

CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;

CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;

CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer

CC activity and can be used to diagnose tumours in mammals, by detecting

CC complex formation when the antibody is contacted with test cells.

CC Increased expression of genes encoding (I) can also be detected to

CC diagnose tumours. Agents which inhibit the activity of (I), especially

CC the antibodies, or an antisense oligonucleotide which hybridises to genes

CC encoding (I), can be used to inhibit tumour growth, preferably by

CC inducing cell death. Methods from the present invention can be used to

CC identify compounds which inhibit the biological activity of (I). AAC58019

CC to AAC58102 represent PCR primers and hybridisation probes used in

CC examples from the present invention for human PRO sequences. AAC58103 to

CC AAC58122 and AAC24021 to AAC24040 represent human PRO polynucleotide and

CC protein sequences given in the exemplification of the present invention

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Db 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Qy 61 DDSYWDNDSESNPCQWKQQLRQLVRKMLRTSETISTVQEKQNTSPLVRERGQ 120

Db 61 DDSYWDNDSESNPCQWKQQLRQLVRKMLRTSETISTVQEKQNTSPLVRERGQ 120

Qy 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

Qy 181 FYIYSQTYFRFQEEIKENTKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240

Db 181 FYIYSQTYFRFQEEIKENTKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 11

AAB08545

ID AAB08545 standard; protein; 281 AA.

XX

AC AAB08545;

XX

DT 20-DEC-2000 (first entry)

XX

XX Amino acid sequence of a human TRAIL polypeptide.

XX

XX Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;

XX TNF related apoptosis-inducing ligand; tumour cell;

XX TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;

XX non-small cell lung carcinoma.

XX

XX Homo sapiens.

XX

XX W0200048619-A1.

XX

XX 24-AUG-2000.

XX

XX 15-FEB-2000; 2000WO-US003891.

XX

XX 16-FEB-1999; 99US-0120313P.

XX

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Rosen GD;

XX WPI; 2000-558253/51.

DR N-PSDB; AAA64325.

XX

PT Killing of tumor cells, e.g. solid tumors or carcinoma, comprises

PT administration of synergistic combination of diterpenoid diepoxide and

PT tumor necrosis factor related apoptosis-inducing ligand.

XX

PS Disclosure; Page 23-24; 29pp; English.

XX

CC The present sequence represents a human TRAIL (tumour necrosis factor

CC (TNF) related apoptosis-inducing ligand) polypeptide. The specification

CC describes a method for enhanced killing of tumour cells. The method

CC comprises contacting a susceptible tumour cell with a synergistic mixture

CC of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined

CC dosage to kill at least 50 % of the cells. This mixture is synergistic,

CC and so is active at lower doses and against otherwise resistant cell

CC lines. The method is used for killing tumour cells, especially solid

CC tumours or carcinomas (especially mammary carcinoma or non-small cell

CC lung carcinoma)

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Db 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Qy 61 DDSYWDNDSESNPCQWKQQLRQLVRKMLRTSETISTVQEKQNTSPLVRERGQ 120

Db 61 DDSYWDNDSESNPCQWKQQLRQLVRKMLRTSETISTVQEKQNTSPLVRERGQ 120

Qy 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

Qy 181 FYIYSQTYFRFQEEIKENTKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240

Db 181 FYIYSQTYFRFQEEIKENTKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 12

AAB28691

ID AAB28691 standard; protein; 281 AA.

XX

AC AAB28691;

XX

DT 14-FEB-2001 (first entry)

XX

XX Human AGP-1.

XX

XX Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;

XX antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;

XX human immunodeficiency virus; apoptosis; proliferative disorder; cancer;

XX hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;

XX transplant rejection; cardiovascular disease; arteriosclerosis.

XX

XX Homo sapiens.

XX

XX W0200063253-A1.

XX

XX 26-OCT-2000.

XX

XX 24-MAR-2000; 2000WO-US008004.

XX PR 16-APR-1999; 99US-00293245.  
 XX PA (AMGE-) AMGEN INC.  
 XX PI Hsu H, Meng S;  
 XX WPI; 2000-665240/64.  
 DR N-PSDB; AAC67831.  
 XX PT Fusion protein of AGP-1 protein and an Fc region, used to treat  
 PT proliferative disorders, immune disorders, and virally-induced disorders.  
 XX PS Claim 3; Fig 2; 93pp; English.  
 XX CC The present sequence is human AGP-1, a type II transmembrane protein.  
 CC Fusion proteins comprising an Fc immunoglobulin region fused to the N-  
 CC terminal portion of the AGP-1 protein have been produced. The fusion  
 CC proteins can be used to induce apoptosis in a tissue, and to treat  
 CC proliferative disorders, immune disorders, or virally-induced disorders.  
 CC The proliferative disorders include cancers, such as breast, prostate,  
 CC lung or colon cancer. The viral infections include hepatitis, and  
 CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may  
 CC be autoimmune disorders or transplant rejection. Cardiovascular diseases  
 CC such as arteriosclerosis may also be treated. The AGP-1 containing fusion  
 CC proteins have increased biological activity compared to the soluble AGP-1  
 CC proteins used in prior art therapies  
 XX SQ Sequence 281 AA;  
 Query Match 100.0%; Score 1478; DB 3; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137; Indels 0; Gaps 0;  
 Matches 281; Conservative 0; Mismatches 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSGIACFLKE 60  
 Db 1 MAMMEVQGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSGIACFLKE 60  
 QY 61 DDSYWDNDDESMNSPCQVQKQRLVRKMLRTSEETISTVQSKQNIISPLVREPGQ 120  
 Db 61 DDSYWDNDDESMNSPCQVQKQRLVRKMLRTSEETISTVQSKQNIISPLVREPGQ 120  
 QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 QY 181 FYIYISQTYFRQBEIKENTKNDKQMVYIYKTSYDPDILLMKSARNCSKDAEYGLY 240  
 Db 181 FYIYISQTYFRQBEIKENTKNDKQMVYIYKTSYDPDILLMKSARNCSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281  
 RESULT 13  
 AAB50977  
 ID AAB50977 standard; protein; 281 AA.  
 XX AC AAB50977;  
 XX DT 21-MAR-2001 (first entry)  
 XX DE Human PRO1096 protein.  
 XX KW Human; PRO; cytostatic; neurotropic; neuroprotective; respiratory general;  
 KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;  
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.  
 XX OS Homo sapiens.  
 XX PN WO200073348-A2.  
 XX

PD 07-DEC-2000.  
 XX 30-MAY-2000; 2000WO-US014941.  
 XX 02-JUN-1999; 99WO-US012252.  
 PR 22-JUN-1999; 99US-0140650P.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 09-DEC-1999; 99US-0170262P.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030999.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US013705.  
 XX (GETH ) GENENTECH INC.  
 PA Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;  
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;  
 XX WPI; 2001-016509/02.  
 DR N-PSDB; AAC91579.  
 XX Twenty eight nucleic acids encoding PRO polypeptides which are useful for  
 PT treating various tumors, e.g. breast cancer, and other inflammatory,  
 PT angiogenic and immunological disorders.  
 XX Claim 31; Fig 54; 188pp; English.  
 XX The present sequence is one of twenty eight novel PRO polypeptides. The  
 CC PRO polypeptides and their agonists, including antibodies, peptides, and  
 CC small molecule agonists, may be used to treat various tumors, e.g.,  
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal  
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,  
 CC central nervous system cancer, melanoma or leukaemia. They are also  
 CC useful for treating other disorders such as neuronal, glial, astrocytal,  
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and  
 CC blastocoealic disorders, and inflammatory, angiogenic and immunological  
 CC disorders  
 XX SQ Sequence 281 AA;  
 Query Match 100.0%; Score 1478; DB 4; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137; Indels 0; Gaps 0;  
 Matches 281; Conservative 0; Mismatches 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSGIACFLKE 60  
 Db 1 MAMMEVQGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSGIACFLKE 60  
 QY 61 DDSYWDNDDESMNSPCQVQKQRLVRKMLRTSEETISTVQSKQNIISPLVREPGQ 120  
 Db 61 DDSYWDNDDESMNSPCQVQKQRLVRKMLRTSEETISTVQSKQNIISPLVREPGQ 120  
 QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 QY 181 FYIYISQTYFRQBEIKENTKNDKQMVYIYKTSYDPDILLMKSARNCSKDAEYGLY 240  
 XX

Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240  
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14  
AAB67243  
ID AAB67243 standard; protein; 281 AA.  
XX AAB67243;  
XX 18-APR-2001 (first entry)  
XX Human Apo2 ligand.  
XX Human; Apo2 ligand: divalent metal ions; viral infection; cancer.  
XX Homo sapiens.  
OS WO200100832-A1.  
PN XX  
XX 04-JAN-2001.  
PD 26-JUN-2000; 2000WO-US017579.  
PF 28-JUN-1999; 99US-0141342P.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;  
PI O'Connell M, Pai R, Shahrokh Z, Simmons L;  
PI WPI; 2001-123012/13.  
XX Use of divalent metal ions for making Apo-2 ligand and in formulations  
PT containing Apo-2 ligand for increasing yield and stability of ligand  
PT trimers, useful for therapeutic applications.  
XX Claim 6; Fig 1; 60pp; English.  
XX The present invention relates to a formulation comprising Apo-2 ligand  
CC and divalent metal ions. Apo-2 ligand and the formulation are useful for  
CC treating cancers and viral infections. Addition of divalent metal ions  
CC for making Apo-2 ligand and formulations containing Apo-2 ligand results  
CC in increased yield and stability of Apo-2 ligand trimers  
XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.8e-137; Mismatches 0; Indels 0; Gaps 0;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTQCVLIIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKGIACFLKE 60  
Db 1 MAMMEVGGPSLGTQCVLIIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKGIACFLKE 60

QY 61 DDSYWDNDSESMNSPCQVQKQLRQLVRKMLRTSBETISTVQEKQNISPLVRERGPO 120  
Db 61 DDSYWDNDSESMNSPCQVQKQLRQLVRKMLRTSBETISTVQEKQNISPLVRERGPO 120

QY 121 RVAAHITGTRSNLTSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180  
Db 121 RVAAHITGTRSNLTSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240  
Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240

QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 15  
AAE11031  
ID AAE11031 standard; protein; 281 AA.  
XX AAE11031;  
XX 18-DEC-2001 (first entry)  
XX Human TNF related apoptosis inducing ligand (TRAIL) protein.  
XX Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;  
KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;  
XX human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;  
XX melanoma.  
XX Homo sapiens.  
OS XX  
XX Key Location/Qualifiers  
FH Domain 1..18  
FT /label= N\_terminal\_cytoplasmic\_domain  
FT Region 19..38  
FT /label= Transmembrane\_region  
FT Domain 39..281  
FT /label= Extracellular\_domain  
XX US6284236-B1.  
XX 04-SEP-2001.  
XX 26-MAY-1999; 99US-00320424.  
XX 29-JUN-1995; 95US-00496632.  
PR 01-NOV-1995; 95US-00548368.  
PR 25-JUN-1996; 96US-00670354.  
PR 26-MAR-1998; 98US-00048641.  
PR 10-NOV-1998; 98US-00190046.  
XX (IMMV ) IMMUNEX CORP.  
XX Wiley SR, Goodwin RG;  
XX WPI; 2001-595463/67.  
DR N-PSDB; AAD18395.  
XX New tumor necrosis factor related apoptosis inducing ligand polypeptides  
PT for treating viral infections (e.g. bovine viral diarrhoea or human  
PT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).  
XX Claim 2; Col 45-48; 41pp; English.  
XX The invention relates to a cytokine designated as tumour necrosis factor  
CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis  
CC of certain target cells, including cancer cells and virally infected  
CC cells. The TRAIL polypeptides are useful in killing cancer cells, in  
CC treating viral infections (e.g. bovine viral diarrhoea or human  
CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and  
CC melanoma), as a research reagent useful in studying apoptosis including  
CC the regulation of programmed cell death. TRAIL DNA sequences may be  
CC employed in developing a gene therapy approach to treating disorders  
CC mediated by defective or insufficient amounts of TRAIL, in the production  
CC of TRAIL polypeptides and as probes or primers in polymerase chain  
CC reactions (PCR). The present sequence is human TRAIL protein  
XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.8e-137; Mismatches 0; Indels 0; Gaps 0;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTQCVLIIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKGIACFLKE 60  
|||

Db 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60  
 QY 61 DSDYNDPNDDESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQONISPLVREGPQ 120  
 Db 61 DSDYNDPNDDESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQONISPLVREGPQ 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180  
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180  
 QY 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSGARNSCWSKDAEYGLY 240  
 Db 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSGARNSCWSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 16  
 AAB48350  
 ID AAB48350 standard; protein; 281 AA.  
 XX  
 AC AAB48350;  
 DT 20-APR-2001 (first entry)  
 XX  
 DE Human TR62 polypeptide.  
 XX  
 KW Tumour necrosis factor; TNF; TNF related receptor; TR6; human; TR62;  
 KW antiinflammatory; immunosuppressive; cerebroprotective; vasotropic;  
 KW antiaesthetic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;  
 KW neuroprotection; antirheumatic; antineoplastic; antidiabetic;  
 KW gene therapy; vaccine; TNF-alpha; bone disease; cancer; TRAIL.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200077191-A1.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 12-JUN-2000; 2000WO-US016134.  
 XX  
 PR 15-JUN-1999; 99US-00333593.  
 XX  
 PA (SMK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;  
 XX  
 DR WPI; 2001-112223/12.  
 XX  
 DR N-PSDB; AAC84745.  
 XX  
 XX New tumor necrosis factor related receptor TR6 polynucleotides and  
 PT polypeptides useful for e.g. for treating chronic and acute inflammation,  
 PT arthritis, septicemia, autoimmune diseases, infection, cancer, bone  
 PT diseases.  
 XX  
 PS Disclosure; Page 26; 47pp; English.

XX The invention relates to a human tumour necrosis factor (TNF) related  
 CC receptor, TR6. TR6 can be expressed by standard recombinant methodology.  
 CC The TR6 polypeptides are useful for treating chronic and acute  
 CC inflammation rheumatoid arthritis, septicemia, autoimmune diseases (e.g.  
 CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.  
 CC host disease, infection, stroke, ischaemia, acute respiratory disease  
 CC syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,  
 CC atherosclerosis, and Alzheimer's disease. These may also be used to  
 CC inhibit production of TNF-alpha and eicosanoids, as research reagents and  
 CC materials for discovering treatments and diagnostics to animal and human  
 CC diseases. The polypeptides may further be used as immunogens to produce  
 CC antibodies immunospecific for the TR6 polypeptides. The polynucleotides  
 CC may also be used as hybridization probes for cDNA and genomic DNA, for  
 CC isolating full-length cDNAs and genomic clones encoding TR6 and of other

CC genes having high sequence similarity to TR6 gene, and for chromosome  
 CC identification. The present sequence represents a human TR62 polypeptide,  
 CC TR62 is also known as TRAIL (TNF-related apoptosis-inducing ligand) and is  
 CC a ligand for the TR62 polypeptide

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137; Indels 0; Gaps 0;  
 Matches 281; Conservative 0; Mismatches 0;

QY 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60  
 Db 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60  
 QY 61 DSDYNDPNDDESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQONISPLVREGPQ 120  
 Db 61 DSDYNDPNDDESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQONISPLVREGPQ 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180  
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNLHLRNGELVIHEKG 180  
 QY 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSGARNSCWSKDAEYGLY 240  
 Db 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSGARNSCWSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 17

ABH08133  
 ID ABH08133 standard; protein; 281 AA.  
 XX  
 AC ABH08133;  
 XX  
 DT 10-SEP-2002 (first entry)  
 XX  
 DE Human TRAIL polypeptide.

XX Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;  
 KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;  
 KW tuberculostatic; cytostatic; human; TRAIL.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200236141-A2.  
 XX  
 PD 10-MAY-2002.  
 XX  
 PF 30-OCT-2001; 2001WO-US044834.  
 XX  
 PR 02-NOV-2000; 2000US-0245721P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.

XX Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;  
 PI Thomas EK;  
 XX WPI; 2002-500114/53.  
 XX Treating an individual suffering from infection, e.g. inflammation,  
 PT chickenpox or AIDS, by administering a combination of dendritic cell  
 PT mobilization factor or maturation agent, T cell enhancing factor and  
 PT antigen-specific T cells.  
 XX  
 PS Disclosure; Page 40-42; 43pp; English.

XX The invention relates to treating an individual at risk for or suffering  
 CC from infection with a pathogenic or opportunistic organism. The method  
 CC involves administering a combination of two to five agents comprising:



XX 16-FEB-1999; 99US-0120313P.  
 PR 20-AUG-1999; 99US-0149989P.  
 XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX Rosen GD, Kao P;  
 XX PI  
 XX PI  
 XX PI  
 DR WPI; 2002-121125/16.  
 DR N-PSDB; ABK13192.  
 XX Use of a synergistic combination of death domain receptor ligands and  
 PT diterpenoid triepoxides for killing of tumor cells.  
 XX  
 XX Disclosure; Col 17-20; 20pp; English.  
 XX  
 CC This invention relates to a novel method for enhanced killing of tumour  
 CC cells comprising contacting a tumour cell with a synergistic combination  
 CC of a death domain receptor ligand and a diterpenoid triepoxide. This  
 CC method has cytostatic activity and works by blocking TNF-alpha mediated  
 CC induction of c-IAP2 and c-IAP1. The method of the invention may be used  
 CC for treating tumours, particularly solid tumours, e.g. carcinoma, mammary  
 CC adenocarcinoma and non-small cell lung carcinoma also neurological  
 CC malignancies, haematological malignancies, e.g. non-Hodgkin's lymphoma,  
 CC chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis  
 CC fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-  
 CC cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid  
 CC lupus erythematosus, lichen planus. The combination may be administered  
 CC with other active agents, e.g. anti-metastatic, anti-tumour or anti-  
 CC angiogenic agents. The potent synergy between the diterpenoids and the  
 CC death domain ligands allows increased killing at equivalent or lower  
 CC doses, and can sensitize otherwise resistant cells. This sequence  
 CC represents the human TNF related apoptosis inducing ligand (TRAIL)  
 CC protein sequence. TRAIL is a death domain receptor used in the used  
 CC method of the invention in combination with diterpenoid triepoxides to  
 CC kill tumours by induction of apoptosis  
 XX  
 SQ Sequence 281 AA;  
 Query Match 100.0%; Score 1478; DB 5; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60  
 DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60  
 QY 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120  
 DB 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120  
 QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 QY 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKARNCSCKDAEYGLY 240  
 DB 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKARNCSCKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 RESULT 20  
 AAM51077  
 ID AAM51077 standard; protein; 281 AA.  
 AC AAM51077;  
 XX  
 DT 30-MAY-2002 (first entry)  
 XX Human Apo-2 ligand (TRAIL).

XX Apo-2 ligand; Apo-2L; TRAIL; human; apoptosis; colorectal cancer; tumour;  
 KW antitumour; therapy.  
 XX Homo sapiens.  
 XX OS  
 XX FH Location/Qualifiers  
 FT Protein  
 FT 114..281  
 XX /note= "Apo-2L polypeptide used in method of Claim 18"  
 XX WO200209755-A2.  
 XX PD 07-FEB-2002.  
 XX PF 27-JUL-2001; 2001WO-US023691.  
 XX PR 27-JUL-2000; 2000US-0221256P.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Escandon E, Fox JA, Kelley SK, Xiang H;  
 XX WPI; 2002-268997/31.  
 DR Use of CPT-11 which is a chemotherapeutic agent of the topoisomerase I  
 PT inhibitor class, and Apo-2 ligand receptor agonist for enhancing  
 PT apoptosis in mammalian cells, or for treating cancer in a mammal.  
 XX Claim 18; Page 79-80; 84pp; English.  
 CC The present sequence is that of human Apo-2 ligand (Apo-2L or TRAIL). The  
 CC invention relates to methods of inducing apoptosis in mammalian cells,  
 CC and especially to the use of Apo-2L receptor agonists and CPT-11 (a  
 CC chemotherapeutic agent of the topoisomerase I inhibitor class) to  
 CC synergistically induce apoptosis in mammalian cells, in particular  
 CC mammalian cancer cells, and especially colorectal cancer cells (claimed).  
 CC The cells may be in cell culture or in a mammal, e.g. a mammal suffering  
 CC from cancer or a condition in which induction of apoptosis in the cells  
 CC is desirable. A claimed method of treating cancer in a mammal comprises  
 CC administering CPT-11 and Apo-2L receptor agonist, where the CPT-11 is  
 CC administered about 6-72 hours prior to administration of the Apo-2L  
 CC receptor agonist. Preferred Apo-2L receptor agonists include Apo-2L  
 CC (especially amino acids 114-281 of the present sequence) and anti-DR4 or  
 CC anti-DR5 receptor antibodies. Exposure of the cancer cells to CPT-11 and  
 CC Apo-2L receptor agonist leads to upregulation of DR4 and DR5 receptors,  
 CC directing the cells towards an apoptotic pathway rather than cell cycle  
 CC arrest and possible DNA repair, thus providing enhanced antitumour  
 CC activity. An example illustrates the synergistic inhibition of tumour  
 CC growth by Apo-2L and CPT-11 in athymic nude mice injected s.c. with human  
 CC COLO205 colon carcinoma cells

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 5; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60  
 DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60  
 QY 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120  
 DB 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120  
 QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 QY 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKARNCSCKDAEYGLY 240  
 DB 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKARNCSCKDAEYGLY 240



Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 21

ABP51954  
 ID ABP51954 standard; protein; 281 AA.

AC ABP51954;  
 DT 09-OCT-2002 (first entry)  
 XX Human Apo-2 ligand protein sequence SEQ ID NO.4.

DE Bacterial host; protease; degp; prc; anti-VEGF antibody; antibody;  
 XX humanised; Apo2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;  
 KW anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;  
 KW anti-CD11a; Fab; Fab'2; Fab'2-leucine zipper fusion; anti-VEGF Fab.  
 XX Homo sapiens.

XX WO200248376-A2.  
 XX 20-JUN-2002.  
 XX 07-DEC-2001; 2001WO-US047581.  
 XX 14-DEC-2000; 2000US-0256162P.  
 XX (GETH ) GENENTECH INC.

XX Chen CY;  
 XX WPI; 2002-583522/62.  
 XX N-PSDB; ABQ73920.

XX Novel Escherichia coli strain useful for producing polypeptide, deficient  
 PT in degp and prc encoding protease, and harboring mutant spr gene, product  
 PT of gene suppresses growth phenotypes of strains harboring prc mutants.  
 XX Example 1; Fig 4; 63pp; English.

XX The present invention describes an Escherichia coli strain (I) deficient  
 CC in chromosomal degp and prc encoding protease Degp and Prc, respectively,  
 CC and harbouring a mutant spr gene, the product of mutant spr gene  
 CC suppresses growth phenotypes exhibited by strains harbouring prc mutants.  
 CC (I) is useful for producing a polypeptide, by culturing (I) comprising  
 CC nucleic acid encoding the polypeptide, which is heterologous to the  
 CC strain, such that the nucleic acid is expressed, and recovering the  
 CC heterologous polypeptide from the strain. The heterologous polypeptide is  
 CC proteolytically sensitive. Culturing of (I) is performed in a fermentor  
 CC under conditions of high- or low-cell density fermentation. The  
 CC polypeptide is recovered from the periplasm or culture medium of the  
 CC strain. The polypeptide is an antibody (humanised or full-length  
 CC antibody) or Apo2 ligand. The antibody is an anti-CD18, anti-vascular  
 CC endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2,  
 CC anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an  
 CC antibody fragment having a light chain (kappa light chain). The antibody  
 CC fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18  
 CC Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper  
 CC fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-  
 CC tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti-  
 CC -CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18  
 CC Fab'2-leucine zipper fusion with a 6-lysine tag. The present sequence  
 CC represents a human Apo-2 ligand amino acid sequence from the present  
 CC invention

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 5; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGFSLGQTCVLIVIFTVLLQSLCAVAVTVYFTNELKOMQDKYSKGIACFLKE 60  
 Db 1 MAMMEVQGFSLGQTCVLIVIFTVLLQSLCAVAVTVYFTNELKOMQDKYSKGIACFLKE 60  
 Qy 61 DDSYWDNDDESNMPCWQVQKWLRLVRLKMLTSEETISTVQEKQONISPLVREGRGPQ 120  
 Db 61 DDSYWDNDDESNMPCWQVQKWLRLVRLKMLTSEETISTVQEKQONISPLVREGRGPQ 120  
 Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHKG 180  
 Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHKG 180  
 Qy 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 22

AAO19095  
 ID AAO19095 standard; protein; 281 AA.

XX AAO19095;  
 XX 22-NOV-2002 (first entry)

XX C neoformans antigen expressing dendritic cell related protein #4.  
 DE Human; fungicide; fungal infection; dendritic cell; antigen;  
 KW Cryptococcus neoformans; vaccine; immunostimulant.

XX Homo sapiens.  
 XX WO200266053-A2.  
 XX 29-AUG-2002.

XX 14-DEC-2001; 2001WO-US048288.  
 XX 04-JAN-2001; 2001US-0259653P.

XX (IMMV ) IMMUNEX CORP.  
 XX Thomas EK;  
 XX WPI; 2002-674896/72.

XX Producing a population of activated, Cryptococcus neoformans antigen-  
 PT presenting dendritic cells for preventing or treating C. neoformans  
 PT infection comprises causing the obtained dendritic cells to present the  
 PT antigen.

XX Disclosure; Page 29-30; 32pp; English.

XX The present invention relates to a method of producing a population of  
 CC activated, Cryptococcus neoformans antigen-presenting dendritic cells,  
 CC comprising causing the obtained dendritic cells to present the antigen  
 CC and maturing the dendritic cells. The activated, C. neoformans antigen-  
 CC expressing dendritic cells are useful for treating, or as vaccines or  
 CC vaccine adjuvants against, C. neoformans infection, or for generating  
 CC antigen-specific T cells. The present sequence is a human protein shown  
 CC in the exemplification of the invention

SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 5; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTQCVLIVFTVLQSLCAVATVYVFTNKLQMDQKYSGKIACFLKE 60  
 DB 1 MAMMEVQGGPSLQGTQCVLIVFTVLQSLCAVATVYVFTNKLQMDQKYSGKIACFLKE 60  
 QY 61 DDSYWDPNDESMNSPCWQVKQLRQVRKMLRTSEETISTVQEKQNNISPLVRERGPO 120  
 DB 61 DDSYWDPNDESMNSPCWQVKQLRQVRKMLRTSEETISTVQEKQNNISPLVRERGPO 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVHEKG 180  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVHEKG 180  
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240  
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

## RESULT 23

AAU79593  
 ID AAU79593 standard; protein; 281 AA.

AC AAU79593;

DT 24-SEP-2002 (first entry)

DE Human TNF-related apoptosis inducing ligand (TRAIL) protein.

KW Human; cytostatic; neuroprotective; immunosuppressive; splice variant;  
 KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;  
 KW TRAIL; apoptosis; programmed cell death; differentiation; development;  
 KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;  
 KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;  
 KW therapeutic; neurodegenerative disease; autoimmune disease; aging;  
 KW chromosome 3q26.

OS Homo sapiens.

Key Location/Qualifiers  
 Domain 1..16  
 FT /note= "Cytoplasmic domain"  
 FT 17..38  
 FT /note= "Transmembrane domain"  
 FT 39..281  
 FT /note= "Extracellular domain"  
 FT 118..256  
 FT /note= "TNF domain"

PN US2002061525-A1.

PD 23-MAY-2002.

PF 16-MAY-2001; 2001US-00855544.

PR 16-MAY-2000; 2000IL-00136156.

PA (YELI/) YELIN R.  
 PA (KHOS/) KHOSRAVI R.  
 PA (SAVI/) SAVITZKY K.

PI Yelin R, Khosravi R, Savitzky K;

DR WPI; 2002-479259/51.

PT New splice variants of tumor necrosis factor-related apoptosis inducing  
 PT ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat  
 PT diseases or disorders associated with low expression of the variants.

PS Disclosure; Fig 9; 29pp; English.

XX

CC The invention discloses isolated, naturally occurring, polypeptide splice  
 CC variants of human tumour necrosis factor (TNF)-related apoptosis inducing  
 CC ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal  
 CC cellular differentiation and development of multicellular organisms.  
 CC Apoptosis is induced by certain cytokines which include TNF and TRAIL  
 CC (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane  
 CC protein which induces apoptosis and nuclear factor-B (NF-B) activation in  
 CC many tissues and cells. Receptors for TRAIL include two death domain  
 CC containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1  
 CC and DcR2, lacking the intracellular signalling death domain. TRAIL,  
 CC induced by type I interferons, induces apoptosis in tumour cells, whereas  
 CC normal cells are relatively resistant without showing significant toxic  
 CC side effects. Thus, TRAIL has the potential to be a very useful  
 CC antitumour agent. The naturally occurring splice variants may differ in  
 CC their cellular distribution, expression levels/timing and activity.  
 CC Determining these factors could provide possible mechanisms for the  
 CC induction of apoptosis of tumours cells. The splice variant polypeptides  
 CC and polynucleotides can be used in gene therapy, to raise antibodies, to  
 CC detect the levels, distribution and ratios of expression of TRAIL, and  
 CC its splice variants, in a biological sample and to identify compounds  
 CC which bind the variant TRAIL products and modulate its activity (agonists  
 CC and antagonists). Pharmaceutical compositions, comprising an expression  
 CC vector or any of the amino acid sequences, are useful for causing a  
 CC cytotoxic effect in cancer cells and for treatment of diseases which can  
 CC be ameliorated, cured or prevented by lowering or raising the level of  
 CC the amino acid sequences. The antibodies may also have a therapeutic  
 CC utility in blocking or decreasing the activity of the TRAIL variant  
 CC products. Diseases that may be treated include cancer, neurodegenerative  
 CC diseases, autoimmune diseases, diseases involved in the non-normal  
 CC development of tissues and aging. TRAIL's gene is located on chromosome  
 CC 3q26. The sequence presented is the wild-type human TNF-related apoptosis  
 CC inducing ligand (TRAIL) protein

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 5; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Mismatches 0; Conservative 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTQCVLIVFTVLQSLCAVATVYVFTNKLQMDQKYSGKIACFLKE 60

DB 1 MAMMEVQGGPSLQGTQCVLIVFTVLQSLCAVATVYVFTNKLQMDQKYSGKIACFLKE 60

QY 61 DDSYWDPNDESMNSPCWQVKQLRQVRKMLRTSEETISTVQEKQNNISPLVRERGPO 120

DB 61 DDSYWDPNDESMNSPCWQVKQLRQVRKMLRTSEETISTVQEKQNNISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVHEKG 180

DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240

DB 181 FYIYSQTYFRFQEEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

## RESULT 24

ABG73861

ID ABG73861 standard; protein; 281 AA.

XX ABG73861;

AC ABG73861;

DT 03-APR-2003 (first entry)

DE Human Apo-2 ligand protein.

XX Human; Apo-2; apoptosis; induce apoptosis; inhibit apoptosis; TNFR;

KW nuclear factor-kappa B; NF-kappa B; Apo-2 ligand; AIDS;

KW tumour necrosis factor receptor; acquired immunodeficiency syndrome;

KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
 KW multiple sclerosis; retinitis pigmentosa; cerebellar degeneration;  
 KW aplastic anaemia; myocardial infarction; stroke; reperfusion injury;  
 KW toxin-induced liver disease; cancer; lupus; herpes virus infection.  
 XX  
 OS Homo sapiens.

Key Location/Qualifiers  
 FH Domain 15..40  
 FT /note= "Transmembrane domain"  
 FT Domain 41..281  
 FT /note= "Extracellular domain"  
 FT Modified-site 109  
 FT /note= "N-glycosylated"

XX US6462176-B1.

XX 08-OCT-2002.

XX PF 11-SEP-1997; 97US-00928069.

XX PR 23-SEP-1996; 96US-0026943P.

XX PA (GETH ) GENENTECH INC.

XX PI Ashkenazi AJ;

XX DR WPI; 2003-173840/17.

XX DR N-PSDB; ABX15469.

XX Novel isolated Apo-3 polypeptide useful for inducing apoptosis in  
 PT mammalian cells, for generating antibodies, in affinity purification  
 PT techniques, and in competitive-type receptor binding assays.

XX Example 4; Fig 4; 52pp; English.

XX The invention relates to an Apo-3 polypeptide having an extracellular  
 CC domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide  
 CC has been found to stimulate or induce apoptotic activity in mammalian  
 CC cells. Human Apo-3 exhibits similarities to the tumour necrosis factor  
 CC receptor (TNFR) family of polypeptides. The invention also relates to a  
 CC chimeric molecule comprising an extracellular domain sequence comprising  
 CC residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The  
 CC Apo-3 polypeptide is useful therapeutically to induce apoptosis in  
 CC mammalian cells. Decreased levels of apoptosis has been associated with  
 CC conditions such as cancer, lupus, and herpes virus infection. Increased  
 CC levels of apoptosis are associated with diseases such as acquired  
 CC immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's  
 CC disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis  
 CC pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial  
 CC infarction, stroke, reperfusion injury, and toxin-induced liver disease.  
 CC The Apo-3 polypeptide is also useful in non-therapeutic applications such  
 CC as in quantitative diagnostic assays as a control against which samples  
 CC containing unknown quantities of Apo-3 may be prepared, in generating  
 CC antibodies, as standards in assays for Apo-3, in affinity purification  
 CC techniques, and in competitive-type receptor binding assays. The chimeric  
 CC molecule is useful therapeutically to inhibit apoptosis or nuclear factor  
 CC -kappa B (NF-kappa B) induction, or as an immunogen for producing anti-  
 CC Apo-3 antibodies. The present sequence represents polypeptide sequence of  
 CC the human Apo-2 ligand protein which is also reported to be involved in  
 CC apoptotic cell death. In the current invention the apoptotic activity of  
 CC the Apo-2 ligand protein was measured on human lymphoid cells

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 6; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVATYVFTNELKQMDQKYSKGIACFLKE 60

Db 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVATYVFTNELKQMDQKYSKGIACFLKE 60

OY 61 DDSYMDPNDDESMNSPCWQVKWLQRLVVRKMLRTSEETISTVQEKQONTISPLVRGPG 120  
 |||||  
 Db 61 DDSYMDPNDDESMNSPCWQVKWLQRLVVRKMLRTSEETISTVQEKQONTISPLVRGPG 120  
 |||||  
 OY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLNGLVHKEG 180  
 |||||  
 Db 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLNGLVHKEG 180  
 |||||  
 OY 181 FYYISQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 |||||  
 Db 181 FYYISQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 |||||  
 OY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 |||||  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 |||||

RESULT 25

ABU10205

ID ABU10205 standard; protein; 281 AA.

XX AC ABU10205;

XX DT 11-AUG-2003 (first entry)

XX DE Human Apo-2 ligand.

XX KW Human; Apo-2 ligand; apoptosis; gene therapy; inflammation; cancer;  
 KW neurodegenerative disease; immunosuppressive; tissue typing.

XX OS Homo sapiens.

XX XX US2003004313-A1.

XX PD 02-JAN-2003.

XX PF 28-MAR-2002; 2002US-00112193.

XX PR 23-SEP-1996; 96US-0026943P.

XX PR 11-SEP-1997; 97US-00928069.

XX PA (GETH ) GENENTECH INC.

XX PI Ashkenazi AJ;

XX DR WPI; 2003-438872/41.

XX DR N-PSDB; ACA61696.

XX New isolated Apo-3 polypeptides, useful for stimulating or inducing  
 PT apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo  
 PT or ex vivo gene therapy techniques.

XX Example 4; Fig 4; 50pp; English.

XX The invention relates to an isolated Apo-3 polypeptide. The Apo-3  
 CC polypeptides are useful for stimulating or inducing apoptotic activity in  
 CC mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy  
 CC techniques. The Apo-3 chimeric molecules are useful for inhibiting  
 CC apoptosis, or as immunogens used in generating antibodies. The  
 CC antagonistic antibodies may be used to block excessive apoptosis, for  
 CC instance in neurodegenerative disease, or to block potential autoimmune/  
 CC inflammatory effects of Apo-3 resulting from NF-kappaB activation. The  
 CC nucleic acid sequences are useful as diagnostics for tissue-specific  
 CC typing, for preparing Apo-3 polypeptides, or for generating transgenic or  
 CC knockout animals. The transgenic or knockout animals are useful in  
 CC developing and screening of therapeutically useful reagents. The present  
 CC sequence represents the amino acid sequence of human Apo-2 ligand

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 6; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLQVAVTVYVFTNELKQMDKYKSGIACFLKE 60  
PR 12-JAN-1999; 99US-0115554P.  
PR 12-JAN-1999; 99US-0115558P.  
PR 20-JAN-1999; 99US-0116533P.  
Db 1 MAMMEVQGGPSIGQTCVLIVIFTVLLQSLQVAVTVYVFTNELKQMDKYKSGIACFLKE 60  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99US-0123618P.  
QY 61 DDSYWDPNDEESMNSPCQVQKWLRLQVLRKMLIRTSSEETISTVQEKQKQNISPLVREGRGP 120  
PR 12-APR-1999; 99US-00284291.  
PR 20-APR-1999; 99WO-US008615.  
Db 61 DDSYWDPNDEESMNSPCQVQKWLRLQVLRKMLIRTSSEETISTVQEKQKQNISPLVREGRGP 120  
PR 27-APR-1999; 99US-0131294P.  
PR 02-JUN-1999; 99WO-US012252.  
QY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHKG 180  
PR 22-JUN-1999; 99US-0140650P.  
PR 23-JUN-1999; 99US-0141037P.  
Db 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHKG 180  
PR 20-JUL-1999; 99US-0144758P.  
PR 25-AUG-1999; 99US-00380137.  
QY 181 FYIYSQYFRQEBIKENTKNDKQVQYIYKTSYPPDILLMKARNSCKSKDAEYGLY 240  
PR 25-AUG-1999; 99US-00380138.  
Db 181 FYIYSQYFRQEBIKENTKNDKQVQYIYKTSYPPDILLMKARNSCKSKDAEYGLY 240  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
PR 09-SEP-1999; 99US-00380913.  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
PR 18-OCT-1999; 99US-00403297.  
PR 29-OCT-1999; 99US-0162506P.  
PR 10-NOV-1999; 99US-00423741.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 09-DEC-1999; 99US-0170262P.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030999.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 08-NOV-2000; 2000US-00709238.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872034.  
PR 01-JUN-2001; 2001US-00872035.  
PR 14-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001US-00882836.  
PR 29-JUN-2001; 2001WO-US019692.  
PR 09-JUL-2001; 2001WO-US021066.  
PR 30-JUL-2001; 2001US-0021735.  
PR 06-AUG-2001; 2001US-00918585.  
PR 09-AUG-2001; 2001US-00924419.  
PR 13-AUG-2001; 2001US-00927796.  
PR 28-AUG-2001; 2001US-00929404.  
PR 29-AUG-2001; 2001US-00941992.  
PR 04-SEP-2001; 2001WO-US027099.  
PR 04-SEP-2001; 2001US-00946374.  
XX (GETH ) GENENTECH INC.  
PA Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;  
XX Shelton DL, Smith V, Watanabe CK, Wood WI;  
PI WPI; 2003-328851/06.  
XX N-FSDB; ACAS8016.  
DR Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for  
XX treating tumor, preferably cancer, or for treating neuronal, glial,  
PT

## RESULT 26

ABU71443

ID ABU71443 standard; protein; 281 AA.

AC ABU71443;

XX

XX 09-JUN-2003 (first entry)

XX Human neoplasia inhibiting PRO polypeptide PRO1096.

DE Human; tumour; cancer; neoplasia; liver cancer; sarcoma; breast cancer;

KW ovarian cancer; renal cancer; colorectal cancer; melanoma;

KW uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;

KW gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;

KW central nervous system cancer; hepatic carcinoma; glioblastoma;

KW neuronal disorder; glial disorder; astrocytal disorder;

KW hypothalamic disorder; glandular disorder; macrophagal disorder;

KW epithelial disorder; stromal disorder; blascoceleic disorder;

KW inflammatory disorder; angiogenic disorder; immunologic disorder.

XX Homo sapiens.

OS

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PT hypothalamic, stromal, inflammatory, angiogenic and immunologic disorders.

XX Claim 32; Fig 54; 186pp; English.

PS The invention relates to an isolated secreted and transmembrane  
 CC polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its  
 CC associated signal peptide or PRO polypeptide extracellular domain with or  
 CC without its associated signal peptide. The PRO polypeptide or an antibody  
 CC binding to it is useful for inhibiting the growth of a tumor cell. A  
 CC competition containing a PRO polypeptide is useful for inhibiting  
 CC neoplastic cell growth or for treating a tumour, preferably cancer (such  
 CC as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,  
 CC bladder, gastric, pancreatic, vulval, thyroid, central nervous system  
 CC cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or  
 CC leukaemia) in a mammal. The PRO polypeptide is useful for identifying its  
 CC agonists. The PRO polypeptide or an antibody binding to it is useful in  
 CC the preparation of a medicament for treating a condition which is  
 CC responsive to the PRO polypeptide or an antibody binding to it. The PRO  
 CC polypeptide or an antibody binding to it is also useful for treating  
 CC neuronal, glial, astrocytic, hypothalamic, glandular, macrophagal,  
 CC epithelial, stromal, blastocoeic, inflammatory, angiogenic and  
 CC immunologic disorders. The present sequence represents the amino acid  
 CC sequence of a PRO polypeptide of the invention

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 6; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137; Indels 0; Gaps 0;  
 Matches 281; Conservative 0; Mismatches 0;

QY 1 MAMVEVGGPSLGTCLVIFVTLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
 DB 1 MAMVEVGGPSLGTCLVIFVTLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
 QY 61 DSYWDPNDESNPCWQVKQLRQLVRKMLTSEETISTVQEKQONISPLVRERGQ 120  
 DB 61 DSYWDPNDESNPCWQVKQLRQLVRKMLTSEETISTVQEKQONISPLVRERGQ 120  
 QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHG 180  
 DB 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHG 180  
 QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 27  
 ABG72738  
 ID ABG72738 standard; protein; 281 AA.

XX AC ABG72738;  
 XX AC ABG72738;  
 DT 17-FEB-2003 (first entry)  
 XX Human TNF-related apoptosis inducing ligand (TRAIL) protein.  
 DE Human; allergic disease; allergy; TNF; TRAIL; diagnosis;  
 KW tumour necrosis factor-related apoptosis inducing ligand;  
 KW atopic skin inflammation.

XX Homo sapiens.  
 XX WO200283946-A1.  
 XX 24-OCT-2002.  
 XX 01-MAR-2002; 2002WO-JP001914.

XX 06-APR-2001; 2001JP-00108631.  
 XX (GENO-) GENOX RES INC.  
 PA (NIGE-) JAPAN GEN AGENCY NATION.

XX Sugita Y, Heishi M, Kagaya S, Gunji S, Tsujimoto G;  
 PI WPI; 2003-093037/08.  
 DR N-PSDB; ABX13715.

XX Measurement of the expression level of TNF related apoptosis inducing  
 PT ligand gene for diagnosis and examination of allergic disease and  
 PT screening agents for allergic disease treatment.  
 XX Disclosure; Page 51-52; 58pp; Japanese.

XX The invention discloses a method for examining allergic diseases, which  
 CC comprises measuring the expression level of tumour necrosis factor (TNF)-  
 CC related apoptosis inducing ligand (TRAIL) gene in a specimen from the  
 CC patient and comparing this level with the level in healthy persons. TRAIL  
 CC gene expression is decreased in patients. The nucleic acids and  
 CC polypeptide can be used to screen for agents for the treatment of  
 CC allergic diseases, possibly using a transgenic rodent as a model animal  
 CC for the disease, with effectiveness determined by changes in expression  
 CC levels or protein activity. The method is useful for the diagnosis,  
 CC examination, prevention and treatment of allergic diseases, including  
 CC atopic skin inflammation. The sequence presented is the human TRAIL  
 CC protein

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 6; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137; Indels 0; Gaps 0;  
 Matches 281; Conservative 0; Mismatches 0;

QY 1 MAMVEVGGPSLGTCLVIFVTLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
 DB 1 MAMVEVGGPSLGTCLVIFVTLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
 QY 61 DSYWDPNDESNPCWQVKQLRQLVRKMLTSEETISTVQEKQONISPLVRERGQ 120  
 DB 61 DSYWDPNDESNPCWQVKQLRQLVRKMLTSEETISTVQEKQONISPLVRERGQ 120  
 QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHG 180  
 DB 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHG 180  
 QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 28  
 AAO29543  
 ID AAO29543 standard; protein; 281 AA.

XX AC AAO29543;  
 XX AC AAO29543;  
 DT 27-AUG-2003 (first entry)  
 XX Human TRAIL protein.  
 DE Human; TNF-related apoptosis-inducing ligand; Kaposi's sarcoma; cancer;  
 KW hyperproliferative disorder; rheumatoid arthritis; Parkinson's disease;  
 KW neurodegenerative disorder; Alzheimer's disease; Hashimoto's disease;  
 KW allergic disorder; acquired immune deficiency syndrome; ocular disorder;  
 KW myasthenia gravis; autoimmune disorder; Huntington's disease; vaccine;  
 KW septic shock; multiple sclerosis; inflammatory disorder; liver injury;



CC The antibody is useful for treating disorders mediated or exacerbated by  
 CC TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic  
 CC thrombocytopenic purpura (TTP), adult haemolytic uraemic syndrome (HUS)  
 CC (even though it can strike children as well) small blood vessel clotting  
 CC disorders e.g., cardiac problems in paediatric AIDS patients and systemic  
 CC lupus erythematosus (SLE). The present sequence represents human TRAIL  
 XX  
 SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 6; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
 DB 1 MAMVEVGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
 QY 61 DDSYDNDDESNMPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120  
 DB 61 DDSYDNDDESNMPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120  
 QY 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
 DB 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 30  
 ABR42313  
 ID ABR42313 standard; protein; 281 AA.  
 XX  
 AC ABR42313;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE Human TRAIL protein.  
 XX  
 KW Human; TRAIL; tumour necrosis factor; ligand; cytostatic;  
 KW immunomodulator; osteopathic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003040307-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 25-JUL-2002; 2002WO-US023782.  
 XX  
 PR 27-JUL-2001; 2001US-0307838P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Hilbert DH, Rosen CA;  
 XX  
 DR WPI; 2003-430659/40.  
 XX  
 DR N-PSDB; ACC57899.  
 XX  
 XX New heteromultimeric complex having a first polypeptide member of the  
 PT tumor necrosis factor (TNF) ligand family, and a second different member  
 PT of TNF ligand family, useful for treating cancer, osteoporosis or an  
 PT autoimmune disease.  
 XX  
 PS Disclosure; Page 364-365; 388pp; English.  
 XX  
 CC The present sequence is the protein sequence of human TRAIL polypeptide.  
 CC The invention relates to compositions comprising heterotrimeric complexes

CC of tumour necrosis factor (TNF) ligand family members, and their use in  
 CC the detection, prevention and treatment of disease. In one embodiment,  
 CC the heterotrimeric complex comprises full-length or extracellular  
 CC portions of TRAIL and full-length or extracellular portions of other TNF  
 CC ligand family members, preferably RANKL. The heterotrimeric complexes of  
 CC the invention are useful for treating an autoimmune disease, cancer or  
 CC osteoporosis, and particularly for inhibiting cancer cell proliferation,  
 CC increasing B cell proliferation, or inducing apoptosis of T cells. A  
 CC claimed method of inducing apoptosis of T cells comprises administering a  
 CC heterotrimeric complex consisting of FasL and LIGHT, TNF-alpha,  
 CC lymphotoxin-beta or TRAIL. A claimed method of inhibiting cancer cell  
 CC proliferation involves administering a heterotrimeric complex consisting  
 CC of TRAIL and CD40L or RANK. A claimed method of treating osteoporosis  
 CC comprises administering an antibody against a complex comprising RANKL  
 CC and TRAIL  
 XX  
 SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 6; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
 DB 1 MAMVEVGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
 QY 61 DDSYDNDDESNMPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120  
 DB 61 DDSYDNDDESNMPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120  
 QY 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
 DB 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 31  
 ABG71905  
 ID ABG71905 standard; protein; 281 AA.  
 XX  
 AC ABG71905;  
 XX  
 DT 20-JAN-2003 (first entry)  
 XX  
 DE Human TRAIL receptor-associated protein.  
 XX  
 KW Human; TRAIL receptor; tumour necrosis factor; TNF;  
 KW light chain variable region TNF-related apoptosis-inducing ligand;  
 KW antibody; VH; VL; cancer; heavy chain variable region; TR4; TR5; TR7;  
 KW TR10; apoptosis; hyperproliferative disorder; hybridoma cell line;  
 KW Kaposi's sarcoma; graft-versus-host disease; GVHD; infectious disease;  
 KW AIDS; acquired immunodeficiency syndrome; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; autoimmune disorder;  
 KW multiple sclerosis; Behcet's disease; lupus erythematosus;  
 KW inflammatory disease; rheumatoid arthritis; psoriasis; wound healing;  
 KW cardiovascular disorder; angiogenesis; immune response;  
 KW chemotherapeutic agent.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200279377-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 07-NOV-2001; 2001WO-US042996.  
 XX

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PR 08-NOV-2000; 2000US-0246612P.
PR 16-NOV-2000; 2000US-0248847P.
PR 27-NOV-2000; 2000US-0252904P.
PR 04-JUN-2001; 2001US-0295018P.
PR 09-OCT-2001; 2001US-0327359P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Salcedo T, Roschke V, Ruben SM, Rosen CA;
XX WIPI; 2003-040669/03.
XX DR
XX PT Novel antibody for treating, or preventing disease or disorder, comprises
XX PT amino acid sequence having identity to other amino acid sequence of
XX PT either variable heavy/light chain-complementarity determining regions.
XX
XX Disclosure; Page 366; 375pp; English.
XX
XX The invention relates to an isolated antibody comprising a first amino
XX acid sequence having 95 % identity to a second amino acid sequence of
XX either variable heavy chain or light chain-complementarity determining
XX regions (VHCDRI)/VHCDRI, VHCDRI/VHCDRI or VHCDRI/VHCDRI appearing as
XX ABG71906-ABG71911 being specific for human TRAIL receptors 1-4 (TNF
XX (tumour necrosis factor)-related apoptosis-inducing ligand receptor, also
XX known as TR4, TR5, TR7 and TR10). Also included are an isolated cell that
XX produces the antibody, an antibody that binds the same epitope on a TR4
XX polypeptide as the antibodies detailed above, detecting expression of a
XX TR4 polypeptide (or detecting, diagnosing, prognosing or monitoring
XX cancers, and other hyperproliferative disorders) using the antibodies, a
XX hybridoma cell line selected from the hybridoma cell lines contained in
XX ATCC Deposit No. PTA-3149, PTA-2687, PTA-3369, PTA-2730, PTA-2729, PTA-
XX 2728, PTA-3368, and PTA-2731 and the antibodies expressed by these
XX hybridoma cell lines. The antibodies of the invention are useful for
XX diagnosing or treating a disease or disorder associated with increased or
XX decreased apoptosis, e.g. cancer (such as colon, breast, uterine,
XX pancreatic, lung, gastrointestinal, and Kaposi's sarcoma), graft-versus-
XX host disease (GVHD), infectious disease, acquired immunodeficiency
XX syndrome (AIDS), or neurodegenerative disorders (e.g. Alzheimer's
XX disease, Parkinson's disease), autoimmune disorders like multiple
XX sclerosis, Behcet's disease, lupus erythematosus, inflammatory diseases
XX such as rheumatoid arthritis, and psoriasis, cardiovascular disorders, in
XX promoting angiogenesis, wound healing, and in regulating immune response.
XX Many other diseases and disorders are listed in the specification. The
XX antibody is administered in combination with a chemotherapeutic agent
XX selected from irinotecan, paclitaxel (TAXOL (RPM)), and gemcitabine. The
XX antibody is useful as a diagnostic tool to monitor the expression of
XX TRAIL receptor expression on cells, to detect, purify, and target the
XX polypeptides, and in immunoassays for qualitatively and quantitatively
XX measuring levels of TRAIL receptor polypeptides. The present sequence is
XX a human TRAIL receptor associated protein. Note: The present sequence is
XX included in the sequence listing but is not referred to anywhere else in
XX the specification
XX
XX Sequence 281 AA;
XX
XX Query Match
XX Best Local Similarity 100.0%; Score 1478; DB 6; Length 281;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNLKQMDKYSGIACFLKE 60
XX DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNLKQMDKYSGIACFLKE 60
XX
XX QY 61 DDSWDNDNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQKQKQNSPLVREGRPQ 120
XX DB 61 DDSWDNDNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQKQKQNSPLVREGRPQ 120
XX
XX QY 121 RVAAHITCTGRSNTLSSPNSKNEKALGRKKNSSSSGHSFSLNHLRNGELVIHFKG 180
XX DB 121 RVAAHITCTGRSNTLSSPNSKNEKALGRKKNSSSSGHSFSLNHLRNGELVIHFKG 180
XX
XX QY 181 FYIYTSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240
XX DB 181 FYIYTSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240
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Db 181 FYIYTSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 32
ABP60546
ID ABP60546 standard; protein; 281 AA.
XX
XX AC ABP60546;
XX
XX DT 28-MAR-2003 (first entry)
XX
XX DE Human tumour necrosis factor TRAIL.
XX
XX KW APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
XX dermatological; immunosuppressive; antiinflammatory; antirheumatic;
XX antiarthritic; cytostatic; antianaemic; antiallergic; antidiabetic;
XX neuroprotective; ophthalmological; tuberculostatic; antidiabetic;
XX antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;
XX haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
XX inflammatory disorder; proliferative disorder; single chain antibody;
XX antibody; human; TRAIL; tumour necrosis factor.
XX
XX OS Homo sapiens.
XX
XX FN WO200294192-A2.
XX
XX PD 28-NOV-2002.
XX
XX PF 22-MAY-2002; 2002WO-US016106.
XX
XX PR 24-MAY-2001; 2001US-0293100P.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Ruben SM;
XX
XX WIPI; 2003-156740/15.
XX
XX Novel isolated antibody that immunospecifically binds tumor necrosis
XX factor delta, useful for treating, preventing or ameliorating Non-
XX Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
XX syndrome.
XX
XX Disclosure; Page 216-217; 225pp; English.
XX
XX The invention relates to a novel antibody or its fragment, which
XX immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).
XX The antibody of the invention has dermatological, immunosuppressive,
XX antiinflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,
XX antiallergic, antidiabetic, neuroprotective, ophthalmological,
XX tuberculostatic, antidiabetic, antipsoriatic, anti-HIV,
XX antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
XX The antibody or its fragment are useful for treating, preventing or
XX ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
XX human, disease or disorder such as autoimmune disease, and graft versus
XX host disease (GVHD). The autoimmune disease is systemic lupus
XX erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
XX is useful for detecting, diagnosing, prognosing, treating, preventing or
XX ameliorating a disease or disorder associated with aberrant APRIL or
XX APRIL receptor expression or aberrant function of APRIL or APRIL
XX receptor. The disease or disorders includes autoimmune and inflammatory
XX disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
XX asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
XX uveitis, tuberculous diabetes mellitus, psoriasis, cancer of the immune
XX system, particularly B cell cancers, immune disorders such as myasthenia
XX gravis, Hashimoto's disease, acquired immunodeficiency syndrome (AIDS), and
XX proliferative disorders (e.g. leukemia). The present sequence represents
XX the tumour necrosis factor TRAIL
```





AC AAO31151;  
XX  
XX  
XX 06-OCT-2003 (first entry)  
XX  
XX Human TNF-related apoptosis-inducing ligand (TRAIL).  
DE Human; protein coordinate data; heavy chain variable domain; VH; cancer;  
KW complementarity determining region; CDR; light chain variable domain; VL;  
KW TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;  
KW DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;  
KW Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;  
KW glioblastoma; graft versus host disease; antibody therapy; nootropic;  
KW AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;  
KW immunosuppressive; neuroprotective; antibody therapy; antibody.  
XX  
XX Homo sapiens.  
XX  
XX WO2003054216-A2.  
XX  
XX  
XX 03-JUL-2003.  
XX  
XX 19-DEC-2002; 2002WO-US040597.  
XX  
XX 20-DEC-2001; 2001US-0341237P.  
XX 05-APR-2002; 2002US-0369877P.  
XX 04-JUN-2002; 2002US-0384828P.  
XX 18-JUL-2002; 2002US-0396591P.  
XX 15-AUG-2002; 2002US-0403370P.  
XX 13-NOV-2002; 2002US-0425737P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;  
XX  
XX WPI; 2003-569250/53.  
XX  
XX New antibody or its fragment, useful for treating, preventing or  
PT ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or  
PT gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host  
PT disease, AIDS.  
XX  
XX Disclosure; Page 297-298; 301pp; English.  
XX  
XX The invention relates to an isolated antibody or its fragments such as  
CC VHCDR1 (heavy chain variable domain complementarity determining region),  
CC VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity  
CC determining region), VLCDR2 or VLCDR3. The antibody or its fragment  
CC immunospecifically binds TRAIL (tumour necrosis factor; TNF-related  
CC apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as  
CC TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The  
CC antibody or its fragment is useful for treating, preventing or  
CC ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or  
CC gastrointestinal cancer or Kaposi's sarcoma or cancer of the central  
CC nervous system such as medulloblastoma, neuroblastoma or glioblastoma or  
CC graft versus host disease, AIDS (acquired immune deficiency syndrome) or  
CC a neurodegenerative disorder. The invention is useful in antibody  
CC therapy. The present sequence is human TRAIL  
XX  
XX Sequence 281 AA;  
SQ  
Query Match 100.0%; Score 1478; DB 6; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCLVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSGGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCLVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSGGIACFLKE 60  
QY 61 DDSDWDPNDEESMNSPCWQVKQLRQMLRTSEETISTVQEKQNI SPLVREGRGP 120  
DB 61 DDSDWDPNDEESMNSPCWQVKQLRQMLRTSEETISTVQEKQNI SPLVREGRGP 120  
QY 121 RVAAHITGTRGSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

DB 121 RVAAHITGTRGSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
QY 181 FYIYISQTYFFRQBEIKENTKDKOMVQYIYKYTSYDPDPILLMKSRNSCWSKDAEYGLY 240  
DB 181 FYIYISQTYFFRQBEIKENTKDKOMVQYIYKYTSYDPDPILLMKSRNSCWSKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASPFAGFLVG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASPFAGFLVG 281  
RESULT 35  
ABO25125  
ID ABO25125 standard; protein; 281 AA.  
XX  
XX ABO25125;  
XX  
XX 05-SEP-2003 (first entry)  
XX  
XX Human TNF-related apoptosis inducing ligand TRAIL Incyte 059509CD1.  
XX  
XX Human; DNA methylation; cancer; colon cancer.  
XX  
XX Homo sapiens.  
XX  
XX US2003013099-A1.  
XX  
XX 16-JAN-2003.  
XX  
XX 07-MAR-2002; 2002US-00093766.  
XX  
XX 19-MAR-2001; 2001US-0277380P.  
XX  
XX (LASE/) LASEK A K W.  
XX (JONE/) JONES D A.  
XX (KARP/) KARP A R.  
XX  
XX Lasek AKW, Jones DA, Karpf AR;  
XX  
XX WPI; 2003-503249/47.  
XX DR N-PSDB; ACD42246.  
XX  
XX New combination comprising cDNAs that are expressed in a disorder or  
PT process associated with DNA methylation, useful for diagnosing, staging,  
PT treating or monitoring treatment of cancer, e.g. colon cancer.  
XX  
XX Disclosure; Page 56-57; 66pp; English.  
XX  
XX The invention relates to a combination comprising cDNAs which are  
CC expressed in a disorder or process associated with DNA methylation. The  
CC combination and cDNAs are useful for diagnosing, staging, treating or  
CC monitoring treatment of cancer, e.g. colon cancer and for detecting  
CC changes in expression of genes encoding proteins that are associated with  
CC DNA methylation. The protein is useful for screening molecules or  
CC compounds to identify at least one ligand that binds to the protein and  
CC for producing an antibody. The present sequence represents the amino acid  
CC sequence of a protein expressed in a disorder or process associated with  
CC DNA methylation  
XX  
XX Sequence 281 AA;  
SQ  
Query Match 100.0%; Score 1478; DB 6; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCLVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSGGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCLVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSGGIACFLKE 60  
QY 61 DDSDWDPNDEESMNSPCWQVKQLRQMLRTSEETISTVQEKQNI SPLVREGRGP 120  
DB 61 DDSDWDPNDEESMNSPCWQVKQLRQMLRTSEETISTVQEKQNI SPLVREGRGP 120  
QY 121 RVAAHITGTRGSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Claim 1; Fig 1; 92pp; English.

The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the DR5.Apo2L complex. The polypeptide having the substitutions made at residue position(s) selected from 20 positions such as S96C, S101C, S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C, R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the residue position is, outside of the receptor contact region of the DR5.Apo2L complex, and displays high solvent accessibility in the crystal structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide and further compositions have the following activities: cytostatic, antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide, an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for inducing apoptosis in mammalian cells, by exposing mammalian cells expressing a receptor selected from DR4 receptor and DR5 receptor to a therapeutically effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,

PT New Endokine alpha gene useful for preparing a composition for treating a  
PT disease associated with excessive or insufficient bone resorption e.g.,  
PT osteoporosis, Paget's disease or arterial calcification.

XX Disclosure; SEQ ID NO 20; 145pp; English.

PS The invention relates to an isolated nucleic acid molecule encoding a

CC tumour necrosis factor family ligand. A composition comprising the

CC isolated antibody or its fragment is used for treating an individual in

CC need of decreased level of endokine alpha activity. The endokine alpha

CC polypeptide present in a heterotrimeric complex is used for treating an

CC individual having a disorder associated with excessive bone resorption,

CC e.g. osteoporosis, Paget's disease or arterial calcification. Treating an

CC individual having a disorder associated with insufficient bone resorption

CC comprises administering an endokine alpha antagonist, which is the

CC antibody that binds specifically to endokine alpha polypeptide. The

CC present sequence represents the amino acid sequence of a tumour necrosis

CC factor family ligand.

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 7; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137; Indels 0; Gaps 0;

Matches 281; Conservative 0; Mismatches 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDESMNSPCQVKWQLRQVLRKMLRTSEETISTVQEKQNI SPLVRGPQ 120

DB 61 DDSYWDPNDESMNSPCQVKWQLRQVLRKMLRTSEETISTVQEKQNI SPLVRGPQ 120

QY 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

DB 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240

DB 181 FYYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 38

ADD14080

ID ADD14080 standard; protein; 281 AA.

XX ADD14080;

XX 01-JAN-2004 (first entry)

XX Human src biomarker polypeptide SEQ ID NO:269.

XX predictor set; protein tyrosine kinase activity modulator;

XX protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;

XX gene therapy; drug sensitivity; genetic profile; cancer; human.

XX Homo sapiens.

XX WO2003062395-A2.

XX 31-JUL-2003.

XX 17-JAN-2003; 2003WO-US001981.

XX 18-JAN-2002; 2002US-0350061P.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Huang F, Fairchild CR, Lee FY, Shaw P;

XX WPI; 2003-636735/60.

XX N-PSDB; ADD14676.

XX New polynucleotides and polypeptides for predicting the activity of

PT compounds that interact with protein tyrosine kinases and/or protein

PT tyrosine kinase pathways.

XX Claim 10; SEQ ID NO 269; 139pp; English.

XX The present invention describes a predictor set comprising a plurality of

CC polynucleotides or polypeptides whose expression pattern is predictive of

CC the response of cells to treatment with a compound that modulates protein

CC tyrosine kinase activity or members of the protein tyrosine kinase

CC pathway. Also described: (1) predicting whether a compound is capable of

CC modulating the activity of cells, comprising obtaining a sample of cells,

CC determining whether the cells express a plurality of markers, and

CC correlating the expression of the markers to the compound's ability to

CC modulate the activity of the cells; (2) a plurality of cell lines for

CC identifying polynucleotides and polypeptides whose expression levels

CC correlate with compound sensitivity or resistance of cells associated

CC with a disease state; and (3) identifying polynucleotides and

CC polypeptides that predict compound sensitivity or resistance of cells

CC associated with a disease state, comprising subjecting the plurality of

CC cell lines to one or more compounds, analysing the expression pattern of

CC a microarray of polynucleotides or polypeptides, and selecting

CC polynucleotides or polypeptides that predict the sensitivity or

CC resistance of cells associated with a disease state by using the

CC expression pattern of the microarray. The polynucleotides and

CC polypeptides have cytostatic activities, and can be used in gene therapy.

CC The polynucleotides and polypeptides are useful in predicting the

CC activity of compounds that interact with protein tyrosine kinases and/or

CC protein tyrosine kinase pathways. These may be used in determining drug

CC sensitivity in patients to allow the development of individualized

CC genetic profiles which aid in treating diseases and disorders (e.g.

CC cancer) based on patient response at a molecular level. The present

CC sequence is used in the exemplification of the present invention.

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 7; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137; Indels 0; Gaps 0;

Matches 281; Conservative 0; Mismatches 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDESMNSPCQVKWQLRQVLRKMLRTSEETISTVQEKQNI SPLVRGPQ 120

DB 61 DDSYWDPNDESMNSPCQVKWQLRQVLRKMLRTSEETISTVQEKQNI SPLVRGPQ 120

QY 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

DB 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240

DB 181 FYYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 39

ADD19010

ID ADD19010 standard; protein; 281 AA.

XX ADD19010;

XX 15-JAN-2004 (first entry)

XX Human disease related protein SeqID499.

XX human; disease state; cytostatic; antiinflammatory; ophthalmological;

KW antiarteriosclerotic; vulnery; gene therapy;  
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;  
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;  
 KW glucose transportation; catecholamine synthesis; iron transport;  
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;  
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;  
 KW inflammatory condition; wound healing.  
 XX Homo sapiens.  
 XX WO2003018621-A2.  
 XX 06-MAR-2003.  
 XX 23-AUG-2002; 2002WO-GB003892.  
 XX 23-AUG-2001; 2001GB-00020558.  
 XX 05-OCT-2001; 2001GB-00024037.  
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.  
 XX Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;  
 DR WPI; 2003-290046/28.  
 DR N-PSDB; ADD19011.  
 XX New substantially purified polypeptide, useful for diagnosing or treating  
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion  
 PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or  
 PT wound healing.  
 XX Claim 25; SEQ ID NO 499; 424pp; English.  
 XX This invention relates to novel human genes and gene product which are  
 CC implicated in certain disease states. Compounds which modulate the  
 CC proteins of the invention may have cytostatic, antiinflammatory,  
 CC ophthalmological, antiarteriosclerotic or vulnerary activities. The  
 CC sequences of the invention may be useful for gene therapy. The invention  
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,  
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,  
 CC erythropoiesis, or the biological response to hypoxia conditions  
 CC including processes such as glycolysis, gluconeogenesis, glucose  
 CC transportation, catecholamine synthesis, iron transport or nitric oxide  
 CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion  
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,  
 CC inflammatory conditions or wound healing. The present sequence is that of  
 CC a disease related protein of the invention.  
 XX SQ Sequence 281 AA;  
 Query Match 100.0%; Score 1478; DB 7; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVQGGPSLQGTCLVIFVTLQSLCAVAVYVFTNELKQMDQKYSKGIACFLKE 60  
 DB 1 MAMMEVQGGPSLQGTCLVIFVTLQSLCAVAVYVFTNELKQMDQKYSKGIACFLKE 60  
 QY 61 DSDYNDPNDSESNPCWQVKQLRQLVRKMLRTSEETISTVQEKQNTSPLVRRGPQ 120  
 DB 61 DSDYNDPNDSESNPCWQVKQLRQLVRKMLRTSEETISTVQEKQNTSPLVRRGPQ 120  
 QY 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLNGLVTHEKG 180  
 DB 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLNGLVTHEKG 180  
 QY 181 FYYISQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSAARNSCWSDAEVGLY 240  
 DB 181 FYYISQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSAARNSCWSDAEVGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 40  
 ABW02276  
 ID ABW02276 standard; protein; 281 AA.  
 XX AC ABW02276;  
 XX 12-FEB-2004 (first entry)  
 XX Human TRAIL protein.  
 XX Gastrointestinal tract disorder; tumour necrosis factor; TNF; DR3; TR6;  
 KW TNF-gamma-beta protein; inflammatory bowel disease; Crohn's disease;  
 KW ulcerative colitis; TRAIL; human.  
 XX Homo sapiens.  
 XX US2003198640-A1.  
 XX 23-OCT-2003.  
 XX 06-DEC-2002; 2002US-00310793.  
 XX 07-NOV-1994; 94WO-US012880.  
 XX 05-JUN-1995; 95US-00461246.  
 XX 09-JAN-1998; 98US-00005020.  
 XX 09-FEB-1998; 98US-0074047P.  
 XX 07-AUG-1998; 98US-00131237.  
 XX 08-FEB-1999; 99US-00246129.  
 XX 30-APR-1999; 99US-0131963P.  
 XX 03-MAY-1999; 99US-0132227P.  
 XX 13-MAY-1999; 99US-0134067P.  
 XX 08-FEB-2000; 2000US-0180908P.  
 XX 27-APR-2000; 2000US-00559290.  
 XX 07-JUL-2000; 2000US-0216879P.  
 XX 26-MAR-2001; 2001US-0278449P.  
 XX 06-JUL-2001; 2001US-00899059.  
 XX 24-AUG-2001; 2001US-0314381P.  
 XX 07-DEC-2001; 2001US-0336895P.  
 XX 23-AUG-2002; 2002US-00228294.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Yu G, Ni J, Rosen CA, Zhang J, Wei P;  
 PI WPI; 2003-852773/79.  
 XX N-PSDB; AAD63912.  
 XX Use of tumor necrosis factor gamma-beta antagonists for treating or  
 PT ameliorating a disease or disorders of the gastrointestinal tract, e.g.  
 PT inflammatory bowel disease, Crohn's disease or ulcerative colitis.  
 XX Disclosure; Page 140-141; Opp; English.  
 XX The invention relates to methods and compositions for treating or  
 CC ameliorating a disease or disorder of the gastrointestinal tract. The  
 CC method involves administering a composition comprising tumour necrosis  
 CC factor (TNF)-gamma-beta and its receptors DR3 and TR6 to a person with,  
 CC or suspected of having the disease or disorder. The antagonist of TNF-  
 CC gamma-beta is useful for treating or ameliorating a gastrointestinal  
 CC tract disease or disorder, specifically an inflammatory bowel disease,  
 CC e.g. Crohn's disease or ulcerative colitis. The present sequence is human  
 CC TRAIL protein. This sequence is used to illustrate the method of the  
 CC invention  
 XX SQ Sequence 281 AA;  
 Query Match 100.0%; Score 1478; DB 7; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLVIFVTLQSLCAVAVYVFTNELKQMDQKYSKGIACFLKE 60

|||||  
1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYKSGIACFLKE 60  
61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQKQNISPLVREGPQ 120  
61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQKQNISPLVREGPQ 120  
121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180  
121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180  
181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 41  
ADE76953  
ID ADE76953 standard; protein; 281 AA.  
AC ADE76953;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human protein expressed in a liver disorder #32.  
XX  
KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;  
KW tumour; liver; inflammatory disorder; immune response disorder;  
KW high-throughput screening; differential gene expression; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2003108871-A1.  
XX  
PD 12-JUN-2003.  
XX  
PF 30-JUL-2001; 2001US-00919039.  
XX  
PR 28-JUL-2000; 2000US-0222113P.  
XX  
PA (KASE/) KASER M R.  
XX  
PI Kaser MR;  
XX  
DR WPI; 2004-031227/03.  
DR N-PSDB; ADE76952.  
XX  
PT Composition comprising several cDNAs that are differentially expressed in  
PT treated human C3A liver cell cultures, useful for treating liver  
PT disorders.  
XX  
PS Claim 1; SEQ ID NO 118; 41pp; English.  
XX  
CC The invention relates to a composition comprising several cDNAs that are  
CC differentially expressed in a liver disorder. The composition is useful  
CC for treating liver disorder such as hyperlipidaemia, hypertension, type  
CC II diabetes, tumours of the liver and disorders of the inflammatory and  
CC immune response. The composition is useful for a high-throughput method  
CC of screening several molecules or compounds to identify a ligand which  
CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a  
CC high-throughput method for using a protein to screen several molecules or  
CC compounds to identify at least one ligand which specifically binds the  
CC protein which involves combining the protein encoded by the cDNA with  
CC several of molecules or compounds under conditions to allow specific  
CC binding, and detecting specific binding between the protein and a  
CC molecule or compound, therefore identifying a ligand which specifically  
CC binds the protein. The composition is useful for detecting and  
CC quantifying differential gene expression, can be used in gene therapy, to  
CC formulate prognosis and to design a treatment regimen and to monitor the

CC efficacy of treatment. The present sequence represents the amino acid  
CC sequence of a protein encoded by a cDNA differentially expressed in a  
CC liver disorder.  
XX  
SQ Sequence 281 AA;  
Query Match 100.0%; Score 1478; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.8e-137; Indels 0; Gaps 0;  
Matches 281; Conservative 0; Mismatches 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYKSGIACFLKE 60  
QY 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQKQNISPLVREGPQ 120  
Db 61 DDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQKQNISPLVREGPQ 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180  
QY 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
Db 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
RESULT 42  
ADK72311  
ID ADK72311 standard; protein; 281 AA.  
XX  
AC ADK72311;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human Apo-2 ligand with potential substitutions highlighted #4.  
XX  
KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;  
KW variant; cancer; immune system disease; arthritis; multiple sclerosis;  
KW human.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FH Misc-difference 189  
FT /note= "wild-type Tyr may be substituted by Ala, Ser or  
FT Xaa (where Xaa is encoded by an amber codon) at this  
FT location in the variant referred to in claim 17"  
FT Misc-difference 191  
FT /note= "wild-type Arg may be substituted by Lys at this  
FT location in the variant referred to in claim 17"  
FT Misc-difference 193  
FT /note= "wild-type Gln may be substituted by Arg at this  
FT location in the variant referred to in claim 17"  
FT Misc-difference 264  
FT /note= "wild-type His may be substituted by Arg, Asp,  
FT Asn, Ala, Pro or Thr at this location in the variant  
FT referred to in claim 17"  
FT Misc-difference 266  
FT /note= "wild-type Ile may be substituted by Val or Leu at  
FT this location in the variant referred to in claim 17"  
FT Misc-difference 267  
FT /note= "wild-type Asp may be substituted by Asn, Glu or  
FT Gln at this location in the variant referred to in claim  
FT 17"  
XX WO2004001009-A2.  
PN 31-DEC-2003.  
XX  
PD

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XX 23-JUN-2003; 2003WO-US019750.
XX
XX 24-JUN-2002; 2002US-0391050P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Hymowitz S, Kelley RF, Lindstrom SH;
XX
XX WPI; 2004-082490/08.
XX
XX New Apo-2 ligand variant polypeptide, useful for preparing a composition
PT for treating cancer or immune-related disease, e.g., arthritis or
PT multiple sclerosis.
XX
XX Claim 17; SEQ ID NO 1; 111pp; English.
XX
XX The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide, comprising a sequence that differs from the native sequence
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having
CC one or more following amino acid substitutions at the residue positions
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand
CC variant polypeptide. Further disclosed are a composition comprising the
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant
CC polypeptide is useful for preparing a composition for treating cancer or
CC immune-related disease, e.g., arthritis or multiple sclerosis. The
CC current sequence represents the human Apo-2 ligand amino acid sequence.
CC Note: The variant sequence that is referred to in claim 17 may contain
CC one or more of the potential substitutions highlighted in the features
CC table for this record.
XX
XX SQ Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1478; DB 8; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-137;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MAMMEVQGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKGIACFLKE 60
DB 1 MAMMEVQGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKGIACFLKE 60
QY 61 DDSYWDPNDESNPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DDSYWDPNDESNPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
DB 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
QY 181 FYYISQTYRFRFOEIKENTKDKQWQVYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
DB 181 FYYISQTYRFRFOEIKENTKDKQWQVYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFLVG 281
XX
RESULT 43
ADK72303
ID ADK72303 standard; protein; 281 AA.
XX
XX ADK72303;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human Apo-2 ligand with potential substitutions highlighted #1.
XX
XX Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;
KW variant; cancer; immune system disease; arthritis; multiple sclerosis;
KW human.
```

```
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 96 /note= "wild-type ser may be substituted for Cys at this
XX location in the variant referred to in claim 1"
XX
XX Misc-difference 101 /note= "wild-type ser may be substituted for Cys at this
XX location in the variant referred to in claim 1"
XX
XX Misc-difference 111 /note= "wild-type ser may be substituted for Cys at this
XX location in the variant referred to in claim 1"
XX
XX Misc-difference 170 /note= "wild-type Arg may be substituted for Cys at this
XX location in the variant referred to in claim 1"
XX
XX Misc-difference 179 /note= "wild-type Lys may be substituted for Cys at this
XX location in the variant referred to in claim 1"
XX
XX WO2004001009-A2.
XX
XX 31-DEC-2003.
XX
XX 23-JUN-2003; 2003WO-US019750.
XX
XX 24-JUN-2002; 2002US-0391050P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Hymowitz S, Kelley RF, Lindstrom SH;
XX
XX WPI; 2004-082490/08.
XX
XX New Apo-2 ligand variant polypeptide, useful for preparing a composition
XX for treating cancer or immune-related disease, e.g., arthritis or
XX multiple sclerosis.
XX
XX Claim 1; SEQ ID NO 1; 111pp; English.
XX
XX The invention relates to a novel isolated Apo-2 ligand variant
XX polypeptide, comprising a sequence that differs from the native sequence
XX Apo-2 ligand polypeptide sequence comprising 282 amino acids and having
XX one or more following amino acid substitutions at the residue positions
XX comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an
XX isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand
XX variant polypeptide. Further disclosed are a composition comprising the
XX Apo-2 ligand variant polypeptide, a method of treating cancer, and a
XX method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant
XX polypeptide is useful for preparing a composition for treating cancer or
XX immune-related disease, e.g., arthritis or multiple sclerosis. The
XX current sequence represents the human Apo-2 ligand amino acid sequence.
XX Note: The variant sequence that is referred to in claim 1 may contain
XX one or more of the potential substitutions highlighted in the features
XX table for this record.
XX
XX SQ Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1478; DB 8; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-137;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MAMMEVQGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKGIACFLKE 60
DB 1 MAMMEVQGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKGIACFLKE 60
QY 61 DDSYWDPNDESNPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DDSYWDPNDESNPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
DB 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
QY 181 FYYISQTYRFRFOEIKENTKDKQWQVYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
DB 181 FYYISQTYRFRFOEIKENTKDKQWQVYIKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFLVG 281
XX
RESULT 43
ADK72303
ID ADK72303 standard; protein; 281 AA.
XX
XX ADK72303;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human Apo-2 ligand with potential substitutions highlighted #1.
XX
XX Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;
KW variant; cancer; immune system disease; arthritis; multiple sclerosis;
KW human.
```

QY 181 FYIYISQTYRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKARNCSKDAEYGLY 240  
|||||  
Db 181 FYIYISQTYRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKARNCSKDAEYGLY 240  
|||||  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
|||||  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
|||||  
RESULT 44  
ADK72304  
ID ADK72304 standard; protein; 281 AA.  
XX  
AC ADK72304;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human Apo-2 ligand with potential substitutions highlighted #2.  
XX  
KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;  
KW variant; cancer; immune system disease; arthritis; multiple sclerosis;  
KW human.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 189  
FT /note= "wild-type Tyr may be substituted by Ala at this  
FT location in the variant referred to in claim 2"  
FT Misc-difference 193  
FT /note= "wild-type Gln may be substituted by Arg, Ser,  
FT Thr, Val or Lys at this location in the variant referred  
FT to in claim 2"  
FT Misc-difference 199  
FT /note= "wild-type Asn may be substituted by Gly, Lys, Val  
FT or Arg at this location in the variant referred to in  
FT claim 2"  
FT Misc-difference 201  
FT /note= "wild-type Lys may be substituted by His, Ala,  
FT Arg, Gly, Thr or Ser at this location in the variant  
FT referred to in claim 2"  
XX  
PN WO2004001009-A2.  
XX  
XX 31-DEC-2003.  
XX  
PF 23-JUN-2003; 2003WO-US019750.  
XX  
PR 24-JUN-2002; 2002US-0391050P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Hymowitz S, Kelley RF, Lindstrom SH;  
XX  
DR WPI; 2004-082490/08.  
XX  
XX New Apo-2 ligand variant polypeptide, useful for preparing a composition  
PT for treating cancer or immune-related disease, e.g., arthritis or  
PT multiple sclerosis.  
XX  
PS Claim 2; SEQ ID NO 1; 111pp; English.  
XX  
CC The invention relates to a novel isolated Apo-2 ligand variant  
CC polypeptide, comprising a sequence that differs from the native sequence  
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having  
CC one or more following amino acid substitutions at the residue positions  
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an  
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand  
CC variant polypeptide. Further disclosed are a composition comprising the  
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a  
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant  
CC polypeptide is useful for preparing a composition for treating cancer or

CC immune-related disease, e.g., arthritis or multiple sclerosis. The  
CC current sequence represents the human Apo-2 ligand amino acid sequence.  
CC Note: The variant sequence that is referred to in claim 2 may contain one  
CC or more of the potential substitutions highlighted in the features table  
CC for this record.  
XX  
SQ Sequence 281 AA;  
Query Match 100.0%; Score 1478; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
|||||  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
|||||  
QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGPQ 120  
|||||  
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGPQ 120  
|||||  
QY 121 RVAAHITCTGRSNTLSSPNSKNEKALORKINSWESSRSGHSFSLNHLRNGELVIHKG 180  
|||||  
Db 121 RVAAHITCTGRSNTLSSPNSKNEKALORKINSWESSRSGHSFSLNHLRNGELVIHKG 180  
|||||  
QY 181 FYIYISQTYRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKARNCSKDAEYGLY 240  
|||||  
Db 181 FYIYISQTYRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKARNCSKDAEYGLY 240  
|||||  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
|||||  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
|||||  
RESULT 45  
ADK72296  
ID ADK72296 standard; protein; 281 AA.  
XX  
AC ADK72296;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human wild-type Apo-2 ligand, seq id 1.  
XX  
KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;  
KW variant; cancer; immune system disease; arthritis; multiple sclerosis;  
KW human.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 119  
FT /note= "Encoded by CCN"  
XX  
PN WO2004001009-A2.  
XX  
XX 31-DEC-2003.  
XX  
XX 23-JUN-2003; 2003WO-US019750.  
XX  
XX 24-JUN-2002; 2002US-0391050P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Hymowitz S, Kelley RF, Lindstrom SH;  
XX  
DR WPI; 2004-082490/08.  
XX  
XX N-PSDB; ADK72297.  
XX  
XX New Apo-2 ligand variant polypeptide, useful for preparing a composition  
PT for treating cancer or immune-related disease, e.g., arthritis or  
PT multiple sclerosis.  
XX  
PS Claim 1; SEQ ID NO 1; 111pp; English.



XX The invention relates to a novel isolated Apo-2 ligand variant  
CC polypeptide, comprising a sequence that differs from the native sequence  
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having  
CC one or more following amino acid substitutions at the residue positions  
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an  
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand  
CC variant polypeptide. Further disclosed are a composition comprising the  
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a  
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant  
CC polypeptide is useful for preparing a composition for treating cancer or  
CC immune-related disease, e.g., arthritis or multiple sclerosis. The  
CC current sequence represents the wild-type human Apo-2 ligand amino acid  
CC sequence.  
XX  
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKGIACFLKE 60  
DB 1 MAMVEVGGPSLGGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKGIACFLKE 60  
QY 61 DDSYWDNDSESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
DB 61 DDSYWDNDSESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
QY 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
DB 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWDAEYGLY 240  
DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 46  
ADK72310  
ID ADK72310 standard; protein; 281 AA.  
XX  
AC ADK72310;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human Apo-2 ligand with potential substitutions highlighted #3.  
XX  
XX Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;  
KW variant; cancer; immune system disease; arthritis; multiple sclerosis;  
KW human.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 189  
FT /note= "wild-type Tyr may be substituted by Ala, Ser, Gln  
FT or Gly at this location in the variant referred to in  
FT claim 10"  
FT  
FT Misc-difference 191  
FT /note= "wild-type Arg may be substituted by Lys or Arg at  
FT this location in the variant referred to in claim 10"  
FT  
FT Misc-difference 193  
FT /note= "wild-type Gln may be substituted by Lys, Arg or  
FT Thr at this location in the variant referred to in Claim  
FT 10"  
FT  
FT Misc-difference 264  
FT /note= "wild-type His may be substituted by Ala, His,  
FT Gly, Gln, Asp, Arg, Pro, Ser, Glu, Asn or Lys at this  
FT

FT Misc-difference 266  
FT location in the variant referred to in claim 10"  
FT /note= "wild-type Ile may be substituted by Leu, Met or  
FT Val at this location in the variant referred to in claim  
FT 10"  
FT  
FT Misc-difference 267  
FT /note= "wild-type Asp may be substituted by Ser, Glu,  
FT Gln, Asp or Asn at this location in the variant referred  
FT to in claim 10"  
FT  
FT Misc-difference 269  
FT /note= "wild-type Asp may be substituted by Ser, Asn,  
FT Asp, Ala, Arg or Glu at this location in the variant  
FT referred to in claim 10"  
FT  
XX WO2004001009-A2.  
XX  
XX 31-DEC-2003.  
XX  
XX 23-JUN-2003; 2003WO-US019750.  
XX  
XX 24-JUN-2002; 2002US-0391050P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Hymowitz S, Kelley RF, Lindstrom SH;  
XX  
XX WPI; 2004-082490/08.  
XX  
XX New Apo-2 ligand variant polypeptide, useful for preparing a composition  
FT for treating cancer or immune-related disease, e.g., arthritis or  
FT multiple sclerosis.  
FT  
XX Claim 10; SEQ ID NO 1; 111pp; English.  
XX  
XX The invention relates to a novel isolated Apo-2 ligand variant  
CC polypeptide, comprising a sequence that differs from the native sequence  
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having  
CC one or more following amino acid substitutions at the residue positions  
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an  
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand  
CC variant polypeptide. Further disclosed are a composition comprising the  
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a  
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant  
CC polypeptide is useful for preparing a composition for treating cancer or  
CC immune-related disease, e.g., arthritis or multiple sclerosis. The  
CC current sequence represents the human Apo-2 ligand amino acid sequence.  
CC Note: The variant sequence that is referred to in claim 10 may contain  
CC one or more of the potential substitutions highlighted in the features  
CC table for this record.  
XX  
XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKGIACFLKE 60  
DB 1 MAMVEVGGPSLGGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKGIACFLKE 60  
QY 61 DDSYWDNDSESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
DB 61 DDSYWDNDSESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
QY 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
DB 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWDAEYGLY 240  
DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

## RESULT 47

ADJ63976

ID ADJ63976 standard; protein; 281 AA.

XX AC ADJ63976;

XX DT 20-MAY-2004 (first entry)

XX DE

XX DE Human apoptosis inducing molecule 1, AIM-1.

XX KW Human; apoptosis inducing molecule 1; AIM-1; apoptosis;  
XX autoimmune disease; graft versus host disease; lymphadenopathy;  
XX immunosuppressive; vasotropic; cytostatic; peripheral tolerance;  
XX cell activation; cell proliferation; immune regulation;  
XX inflammatory response; systemic lupus erythematosus;  
XX immunoproliferative disease; neoplasm; tumour; restenosis.

XX OS Homo sapiens.

XX FH Key

XX FT Peptide

XX FT Location/Qualifiers

XX FT 1..38

XX FT /note= "Signal peptide"

XX FT Protein

XX FT 39..281

XX FT /label= Mature AIM\_1

XX FT /note= "Claimed in claim 1"

XX PN US2004038347-A1.

XX PD 26-FEB-2004.

XX PF 16-SEP-2003; 2003US-00662429.

XX PR 14-MAR-1996; 96US-0013405P.

XX PR 13-MAR-1997; 97US-00816981.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX PA

XX PI Ruben SM;

XX DR WPI; 2004-203230/19.

XX DR N-PSDB; ADJ63975.

XX PT Novel apoptosis inducing molecule polypeptide that induces apoptosis of  
XX cell line derived from pathological tissue and induces apoptosis of T  
XX cells, useful for treating lymphadenopathy, autoimmune diseases and graft  
XX versus host disease.

XX PS Claim 1; SEQ ID NO 2; 36pp; English.

XX CC The invention relates to apoptosis inducing molecule-I protein (AIM-I)  
XX comprising sequence that is 70 % identical to ADJ63976 or its mature form  
XX where the polypeptide binds antibody specific to AIM-1, induces apoptosis  
XX of cell line derived from pathological tissue and induces apoptosis of T  
XX cells. Also included are a composition comprising AIM-1 and a carrier,  
XX AIM-1 produced by a process involving expressing in a host cell a nucleic  
XX acid that encodes the protein so as to produce the protein (where the  
XX nucleic acid is chosen from a polynucleotide encoding AIM-1, mature AIM-  
XX 1, mature AIM-1 except for 1-5 or 5-10 conservative amino acid  
XX substitutions, the amino acid sequence encoded by human cDNA contained in  
XX ATCC deposit No. 97448, and a polynucleotide that is complementary to  
XX polynucleotide which hybridises at 60degreesC in a hybridisation buffer  
XX consisting of 0.5 X SSC (Saline-Sodium Citrate) and 0.1 % sodium dodecyl  
XX sulphate (SDS) to a polynucleotide chosen from polynucleotide encoding  
XX mature AIM 1, and a polynucleotide encoding amino acid sequence encoded  
XX by human cDNA contained in ATCC deposit No. 97448, where the  
XX polynucleotide encodes a polypeptide that has the same biological  
XX activity as described above). AIM-1 is useful for treating  
XX lymphadenopathy, autoimmune diseases, graft versus host disease, for  
XX stimulating peripheral tolerance, destroying pathologic transformed cell

CC lines, mediating cell activation and proliferation. AIM-1 proteins are  
CC functionally linked as primary mediators of immune regulation and  
CC inflammatory response, are useful for diagnosis and treatment of  
CC disorders of cells, tissues and organisms. AIM-1 is useful as research  
CC tool in elucidating biology of autoimmune disorders including systemic  
CC lupus erythematosus, immunoproliferative disease lymphadenopathy and is  
CC useful for inhibiting neoplasia such as tumour cell growth. AIM-1 is also  
CC useful to treat diseases which required growth promotion activity e.g.,  
CC restenosis. AIM-1 is useful for assessing AIM-1 binding capacity of its  
CC binding molecules such as receptor molecules. The present sequence  
CC represents AIM-1.

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVVYFTNELKQMDKYSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVVYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYNDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGPQ 120

DB 61 DDSYNDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGPQ 120

QY 121 RVAAHITGTRGRSNTLSPPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHKG 180

DB 121 RVAAHITGTRGRSNTLSPPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHKG 180

QY 181 FYYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYDPDILLMKSARNSCKDAEYGLY 240

DB 181 FYYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYDPDILLMKSARNSCKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 48

ADL71816

ID ADL71816 standard; protein; 281 AA.

XX AC ADL71816;

XX DT 03-JUN-2004 (first entry)

XX DE Human apoptosis inducing molecule-I (AIM-I) protein.

XX KW Apoptosis inducing molecule-I; AIM-I; cell activation;

XX KW cell differentiation; apoptosis; autoimmune disease;

XX KW graft-versus-host disease; lymphadenopathy; gene therapy; human.

XX OS Homo sapiens.

XX OS US2004047864-A1.

XX PD 11-MAR-2004.

XX PF 16-SEP-2003; 2003US-00662431.

XX PR 14-MAR-1996; 96US-0013405P.

XX PR 13-MAR-1997; 97US-00816981.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX XX Ruben SM;

XX DR WPI; 2004-226168/21.

XX DR N-PSDB; ADL71815.

XX PT New antibodies specific to apoptosis inducing molecule I polypeptides  
XX useful in research, biological, diagnostic, clinical or therapeutic

PT applications, such as in the treatment of autoimmune diseases or graft-versus-host disease.

PS Claim 1; SEQ ID NO 2; 36pp; English.

XX The invention relates to antibodies specific to apoptosis inducing molecule-1 (AIM-1) polypeptides. The invention is useful in research, biological, diagnostic, clinical or therapeutic applications. It is also used for modulating activation and differentiation of cells, both normally and in disease states, or for mediating apoptosis and preventing or treating autoimmune diseases, graft-versus-host disease or lymphadenopathy. The invention is also useful in gene therapy. The present sequence is human AIM-1 protein.

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
 Db 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Qy 61 DDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSETISTVQEKQONISPLVRGPQ 120  
 Db 61 DDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSETISTVQEKQONISPLVRGPQ 120

Qy 121 RVAAHITGRSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180  
 Db 121 RVAAHITGRSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

Qy 181 FYIYSOTYFRFOEIKENTKNDKQWQYIYKYTSYDPPILLMKSARNSCWSDAEYGLY 240  
 Db 181 FYIYSOTYFRFOEIKENTKNDKQWQYIYKYTSYDPPILLMKSARNSCWSDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

# RESULT 49

ID ADK15498 standard; protein; 281 AA.

XX AC ADK15498;

DT 03-JUN-2004 (first entry)

XX Human TRAIL protein.

KW Human; TRAIL; TNF related apoptosis inducing ligand; apoptosis; cytostatic; virucide; tumour necrosis factor; Jurkat cell; cancer; programmed cell death; leukaemia; colorectal cancer; viral infection; vaccine.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..18

FT /note= "Cytoplasmic domain"

FT Domain 19..38

FT /note= "Transmembrane domain"

FT Domain 39..281

FT /note= "Extracellular domain claimed in claim 4"

FT Region 95..281

FT /note= "Claimed in claim 7"

XX US2004052788-A1.

PN 18-MAR-2004.

XX 02-SEP-2003; 2003US-00652244.

XX RESULT 50

XX 29-JUN-1995; 95US-00496632.  
 PR 01-NOV-1995; 95US-00548368.  
 PR 25-JUN-1996; 96US-00670354.  
 PR 26-MAR-1998; 98US-00048641.  
 PR 10-NOV-1998; 98US-00190046.  
 PR 26-MAY-1999; 99US-00320424.  
 PR 27-FEB-2001; 2001US-00796581.  
 XX (IMMV ) IMMUNEX CORP.

XX Willey SR, Goodwin RG;

XX WPI; 2004-238577/22.

XX DR N-PSDB; ADK15497.

XX New tumor necrosis factor related apoptosis inducing ligand polypeptides, useful in studies of apoptosis, in regulating programmed cell death, or for treating leukemia, cancer (e.g. colorectal cancer) or viral infections.

XX Claim 2; SEQ ID NO 2; 42pp; English.

XX The invention relates to a new purified tumour necrosis factor related apoptosis inducing ligand (TRAIL) polypeptide comprising an amino acid sequence that is at least 90% identical to human TRAIL (ADK15498) or mouse TRAIL (ADK15502). The TRAIL polypeptide induces apoptosis of Jurkat cells. Also included are a purified human TRAIL polypeptide encoded by the cDNA insert of the recombinant vector deposited in strain ATCC 69849 (or a fragment of human TRAIL protein of SEQ ID NO: 2 that induces apoptosis of Jurkat cells), a fusion protein comprising a leucine zipper peptide and a soluble TRAIL polypeptide (comprising the extracellular domain) and a leucine zipper comprising ADK15510-ADK15513, an oligomer comprising at least two soluble TRAIL polypeptides (or at least two fusion proteins defined above), an antibody that specifically binds a TRAIL protein above and a method of inducing death of cancer cells (by contacting TRAIL-sensitive cancer cells with a TRAIL polypeptide or with an oligomer defined above). The TRAIL polypeptide is useful in studies of apoptosis, in regulating programmed cell death, for treating leukaemia, cancer (e.g. colorectal cancer) or viral infections, or in purifying leukaemic cells or a desired cell surface antigen which can be used in vaccine development. The TRAIL polypeptide may also be used in developing treatments for any disorder mediated by defective or insufficient amounts of TRAIL. The present sequence represents human TRAIL.

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Db 1 MAMMEVGGPSLGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Qy 61 DDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSETISTVQEKQONISPLVRGPQ 120

Db 61 DDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSETISTVQEKQONISPLVRGPQ 120

Qy 121 RVAAHITGRSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

Db 121 RVAAHITGRSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

Qy 181 FYIYSOTYFRFOEIKENTKNDKQWQYIYKYTSYDPPILLMKSARNSCWSDAEYGLY 240

Db 181 FYIYSOTYFRFOEIKENTKNDKQWQYIYKYTSYDPPILLMKSARNSCWSDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

ADN07587	ID	ADN07587 standard; protein; 281 AA.
XX	AC	ADN07587;
XX	DT	17-JUN-2004 (first entry)
XX	DE	Human apoptosis inducing molecule-1 protein.
XX	KW	Apoptosis inducing molecule I; AIM-I; therapeutic; autoimmune disorder;
XX	KW	systemic lupus erythematosus;
XX	KW	immunoproliferative disease lymphadenopathy; IPL;
XX	KW	angioimmunoproliferative lymphadenopathy; AIL; rheumatoid arthritis;
XX	KW	diabetes; multiple sclerosis; graft versus host disease;
XX	KW	lymphoproliferative disease; lymphadenopathy; neoplasia;
XX	KW	tumour cell growth; restenosis; haematopoiesis;
XX	KW	chromosome identification; pancreatic tumour; endometrial tumour;
XX	KW	T-cell lymphoma; gene therapy; human.
XX	OS	Homo sapiens.
XX	PN	US2004048340-A1.
XX	PD	11-MAR-2004.
XX	PF	16-SEP-2003; 2003US-00662430.
XX	PR	14-MAR-1996; 96US-0013405P.
XX	PR	13-MAR-1997; 97US-00816981.
XX	PA	(HUMA-) HUMAN GENOME SCI INC.
XX	PI	Ruben SM;
XX	DR	WPI; 2004-238497/22.
XX	DR	N-PSDB; ADN07586.
XX	PT	Novel human apoptosis inducing molecule I useful for treating
XX	PT	lymphadenopathy, systemic lupus erythematosus, rheumatoid arthritis and
XX	PT	multiple sclerosis.
XX	PS	Claim 1; SEQ ID NO 2; 35pp; English.
XX	CC	The present invention relates to apoptosis inducing molecule I (AIM-I)
XX	CC	polypeptide and the encoding polynucleotide useful in biological,
XX	CC	diagnostic, clinical and therapeutic arts. The invention is useful in
XX	CC	treating autoimmune disorders such as systemic lupus erythematosus,
XX	CC	immunoproliferative disease lymphadenopathy (IPL),
XX	CC	angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
XX	CC	diabetes and multiple sclerosis, graft versus host disease,
XX	CC	lymphoproliferative disease such as lymphadenopathy, in inhibiting
XX	CC	neoplasia such as tumour cell growth, in treating restenosis and
XX	CC	regulating haematopoiesis in endothelial cell development. The invention
XX	CC	is useful in chromosome identification and as a diagnostic marker for
XX	CC	determining expression of AIM-I polypeptide in tumour cell lines
XX	CC	including pancreatic tumour, endometrial tumour and T-cell lymphoma. The
XX	CC	invention is also useful in gene therapy. The present sequence is human
XX	CC	apoptosis inducing molecule I (AIM-I) protein.
XX	SQ	Sequence 281 AA;
	Query Match	100.0%; Score 1478; DB 8; Length 281;
	Best Local Similarity	100.0%; Pred. No. 3.8e-137;
	Matches 281; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	MAMMEVGGPSLGTQCVLIIVFTVLQLSCVAATVVYFNTNELKMQDKYSKGIACTFLKE 60 
Dd	1	MAMMEVGGPSLGTQCVLIIVFTVLQLSCVAATVVYFNTNELKMQDKYSKGIACTFLKE 60 
Qy	61	DDSYWDPNDEESMNSPCWQVKQROLVRKMILRTSEETISTVQSKQNISPLVREPGPQ 120 
Dd	61	DDSYWDPNDEESMNSPCWQVKQROLVRKMILRTSEETISTVQSKQNISPLVREPGPQ 120 

CC or diseases associated with the NF-kappaB pathway. The condition is an  
 CC immune disorder, an inflammatory disorder, an inflammatory disorder  
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,  
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM  
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic  
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,  
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell  
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory  
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick  
 CC syndrome, stroke, BAE, autoimmune disorders, disorders related to hyper  
 CC immune activity, disorders related to aberrant acute phase responses,  
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,  
 CC organ transplant rejection, conditions related to organ transplan  
 CC rejection, disorders related to aberrant signal transduction,  
 CC proliferating disorders, cancers and HIV propagation in cells infected  
 CC with other viruses. The present sequence is that of a human protein which  
 CC is subject to the novel association with the NF-kappaB pathway of the  
 CC invention. Note: This sequence does not appear in the specification but  
 CC was obtained by the indexer from Genbank.

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGTCLVIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
 DB 1 MAMVEVGGPSLGTCLVIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
 QY 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNIISPLVRGPQ 120  
 DB 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNIISPLVRGPQ 120  
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
 QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 52.

ADK82215  
 ID ADK82215 standard; protein; 281 AA.

XX AC ADK82215;

XX AC ADK82215;

DT 18-NOV-2004 (first entry)

XX Human TRAIL amino acid sequence SEQ ID NO:66.

XX antibody; VH domain; VL domain; TR4 binding antibody; TRAIL receptor;  
 KW haematological cancer; cytostatic; immunotherapy; Non-Hodgkin's lymphoma;  
 KW chronic myelogenous lymphoma; multiple myeloma;  
 KW chronic lymphocytic leukaemia; scFv; human; TRAIL;  
 KW TNF-related apoptosis-inducing ligand.

XX Homo sapiens.

XX WO2004016753-A2.

XX 26-FEB-2004.

XX 15-AUG-2003; 2003WO-US025457.

XX 15-AUG-2002; 2002US-0403382P.

PR 13-NOV-2002; 2002US-0425730P.

PR 06-MAY-2003; 2003US-0468050P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Salcedo T, Ruben SM, Rosen CA, Albert VA;

XX WPI; 2004-203784/19.

XX Use of an antibody or its fragment the specifically binds to TR4, for the  
 XX preparation of a pharmaceutical composition for treating or preventing  
 XX hematological cancer, e.g. Non-Hodgkin's lymphoma, multiple myeloma or  
 XX leukemia.

XX Disclosure; SEQ ID NO 66; 353pp; English.

XX The present invention describes an antibody or its fragment comprising a  
 XX VH and VL domain that is at least 80% identical to a VH and a VL domain  
 XX of any of the 14 sequences given in SEQ ID NO:43 to 56, or a VH and a VL  
 XX domain of an antibody expressed by any one of the cell lines contained in  
 XX American Type Culture Collection (ATCC) Deposit numbers PTA-3571, PTA-  
 XX 3570 and PTA-3675, where the antibody specifically binds TR4 (TRAIL  
 XX receptor). Also described is a pharmaceutical composition for treating or  
 XX preventing haematological cancer, comprising the antibody or its fragment  
 XX and a member selected from ibritumomab tiuxetan, imatinib mesylate,  
 XX bortezomid, and a smac peptide or polypeptide. The antibody has  
 XX its fragment can be used for the preparation of a pharmaceutical  
 XX composition for treating or preventing haematological cancer, e.g. Non-  
 XX Hodgkin's lymphoma, chronic myelogenous lymphoma, multiple myeloma, or  
 XX chronic lymphocytic leukaemia. The present sequence represents human  
 XX tumour necrosis factor (TNF) related apoptosis-inducing ligand (TRAIL),  
 XX which is used in the exemplification of the present invention.

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 8; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGTCLVIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
 DB 1 MAMVEVGGPSLGTCLVIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
 QY 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNIISPLVRGPQ 120  
 DB 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNIISPLVRGPQ 120  
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
 QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 53

ADSS8000

ID ADS88000 standard; protein; 281 AA.

XX AC ADS88000;

XX 18-NOV-2004 (first entry)

XX Tumour treatment-related human protein sequence SeqID36.

XX tumour inhibition; tumour treatment; metastasis; infectious lesion;  
 KW antigen presenting cell; immunostimulatory cytokine; cytostatic;  
 KW vulnery; immunomodulator; melanoma; hepatoma; adenocarcinoma;

KW colorectal cancer; basal cell cancer; oral cancer; nasopharyngeal cancer;  
 KW laryngeal cancer; bladder cancer; head cancer; neck cancer;  
 KW renal cell cancer; pancreatic cancer; pulmonary cancer; cervical cancer;  
 KW ovarian cancer; oesophageal cancer; gastric cancer; prostate cancer;  
 KW testicular cancer; breast cancer; human.

XX Homo sapiens.  
 XX WO2004034995-A2.  
 XX 29-APR-2004.  
 XX 15-OCT-2003; 2003WO-US032827.  
 XX 15-OCT-2002; 2002US-0418865P.  
 XX (UYPI-) UNIV PITTSBURGH.  
 XX Lotze MT, Tahara H;  
 XX WPI; 2004-365083/34.  
 XX N-PSDB; ADS87999.

Inhibiting or treating a tumor, metastasis or infectious lesion comprises administering into or near site of a tumor or infectious lesion an antigen presenting cell and an immunostimulatory cytokine or a nucleic acid encoding the cytokine.

Disclosure; SEQ ID NO 36; 169pp; English.

This invention relates to a novel method of inhibiting or treating a tumor, metastasis or infectious lesion in a subject which comprises administering into or near a site of a tumor or infectious lesion in a subject an antigen presenting cell and an immunostimulatory cytokine or a nucleic acid encoding the cytokine. The invention may be useful for the production of compounds with a cytostatic or cytotoxic activity acting as immunomodulators. The method is useful in inhibiting or treating a tumor, metastasis or infectious lesion in a subject, where the size of the tumor, metastasis (where number is also decreased) or infectious lesion is decreased. The tumor is selected from melanoma, hepatoma, adenocarcinoma, colorectal cancer, basal cell cancer, oral cancer, nasopharyngeal cancer, laryngeal cancer, bladder cancer, head and neck cancer, renal cell cancer, pancreatic cancer, pulmonary cancer, cervical cancer, ovarian cancer, oesophageal cancer, gastric cancer, prostate cancer, testicular cancer and breast cancer. The present sequence is that of a protein which is related to the invention.

Sequence 281 AA;

Query Match	100.0%;	Score 1478;	DB 8;	Length 281;
Best Local Similarity	100.0%;	Pred. No. 3.8e-137;		
Matches 281;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

  

QY	1	MAMBEVQGPSLQGTCLVLI	FTVLLQSLQSLVAVTVYVFTNELKQMDKYSGIACFLKE	60
DB	1	MAMBEVQGPSLQGTCLVLI	FTVLLQSLQSLVAVTVYVFTNELKQMDKYSGIACFLKE	60
QY	61	DDSYWDPNDESMNSPCWQV	KQLRQLVRKMLRTSEETISTVQSKQNI	SPLVREPGQ 120
DB	61	DDSYWDPNDESMNSPCWQV	KQLRQLVRKMLRTSEETISTVQSKQNI	SPLVREPGQ 120
QY	121	RVAAHITCTGRSNTLSSP	NSKNEALGRKKNWESSRSGHSFSLNHLRNGELVHBEKG	180
DB	121	RVAAHITCTGRSNTLSSP	NSKNEALGRKKNWESSRSGHSFSLNHLRNGELVHBEKG	180
QY	181	FYIYSQTYFRQBEIKENT	KNDKQVQYIYKITSYDPDILLMKSRNSCKDAEYGLY	240
DB	181	FYIYSQTYFRQBEIKENT	KNDKQVQYIYKITSYDPDILLMKSRNSCKDAEYGLY	240
QY	241	SIYQGGIFELKENDRIFV	SVTNEHLIDMDHEASFFGAFVNG	281
DB	241	SIYQGGIFELKENDRIFV	SVTNEHLIDMDHEASFFGAFVNG	281

RESULT 54

AB084415  
 ID AB084415 standard; protein; 281 AA.  
 XX AC AB084415;  
 XX DT 18-NOV-2004 (first entry)  
 XX DE Human cancer-associated protein HP7-053.3.  
 XX KW Human; cancer-associated protein; cytostatic; cancer; leukaemia;  
 XX KW lymphoma; CAP.  
 XX OS Homo sapiens.  
 XX PN WO2004074320-A2.  
 XX PD 02-SEP-2004.  
 XX PF 17-FEB-2004; 2004WO-US004730.  
 XX PR 14-FEB-2003; 2003US-00367094.  
 XX PR 15-APR-2003; 2003US-00388838.  
 XX PR 15-APR-2003; 2003US-00417375.  
 XX PR 13-JUN-2003; 2003US-00461862.  
 XX PR 15-SEP-2003; 2003US-00663431.  
 XX PR 15-DEC-2003; 2003US-00737318.  
 XX PA (SAGR-) SAGRES DISCOVERY INC.  
 XX PI Morris DW, Morris DW, Malandro MS;  
 XX WPI; 2004-652914/63.  
 XX N-PSDB; ABD32555.

New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.  
 claim 18; seqid 36; 310pp; English.

The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancer-associated proteins. Also included are an expression vector comprising the isolated nucleic acid or expression vector, a microarray for detecting a cancer-associated (CA) nucleic acid comprising at least one probe comprising at least 10 contiguous nucleotides of any of the above-mentioned nucleotide sequences, an isolated polypeptide (encoded within an open reading frame of a CA sequence selected from any of the 95 polynucleotide sequences as mentioned in the specification, or its complement), an isolated antibody, (or its antigen binding fragment) that binds to the above polypeptide, a hybridoma that produces the above monoclonal antibody, a pharmaceutical composition comprising the above antibody and a pharmaceutical excipient, a kit for detecting cancer cells comprising the antibody cited above, methods for diagnosing cancer or for detecting the presence or absence of cancer cells in an individual, a method for inhibiting growth of cancer cells in an individual, a method for delivering a therapeutic agent to cancer cells in an individual, an electronic library comprising the above polynucleotide or polypeptide (or their fragments), methods of screening for anticancer activity or for a bioactive agent capable of modulating the activity of a CA protein (CAP), methods for detecting cancer associated with expression of a polypeptide in a test cell sample, a method for treating cancers and a method for inhibiting the expression of CA gene in a cell. The composition and methods are useful for detecting, diagnosing, preventing and treating cancers, especially lymphoma and leukaemia. These may also be used in screening for agents that modulate cancer. The present sequence is a human CAP protein sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

```
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVIFVTLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCLVIFVTLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSETSTVQEKQNTSPLVRERG 120
DB 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSETSTVQEKQNTSPLVRERG 120

QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180

QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 55
ADP23388
ID ADP23388 standard; protein; 281 AA.
XX AC ADP23388;
XX DT 18-NOV-2004 (first entry)
XX DE PRO polypeptide SEQ ID NO:566.
XX KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
XX KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
XX KW antiaesthetic; hepatotropic; respiratory; gene therapy; immune system.
XX OS Unidentified.
XX PN WO2004041170-A2.
XX PD 21-MAY-2004.
XX PF 30-OCT-2003; 2003WO-US034312.
XX PR 01-NOV-2002; 2002US-0423394P.
XX PA (GETH ) GENENTECH INC.
XX PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
XX PI Wu TD;
XX DR WPI; 2004-419628/39.
XX DR N-PSDB; ADP23387.
XX PT New PRO polypeptides and polynucleotides, useful for treating e.g.
XX PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
XX PT renal disease, or demyelinating diseases of the central or peripheral
XX PT nervous system.
XX PS Claim 7; SEQ ID NO 566; 2940pp; English.
XX CC The invention relates to a novel isolated nucleic acid and the PRO
XX CC polypeptide encoded by it. A protein of the invention has
XX CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
XX CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
XX CC antiaesthetic, hepatotropic, and respiratory activity. A polynucleotide
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CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polynuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX SQ Sequence 281 AA;
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Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAMMEVGGPSLGGTCLVIFVTLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSETSTVQEKQNTSPLVRERG 120
DB 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSETSTVQEKQNTSPLVRERG 120

QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180

QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2005, 11:53:43 ; Search time 54 Seconds  
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1798.816 Million cell updates/sec

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Perfect score: 1478  
Sequence: 1 MAMMEVQGSLSGTCVLIV.....NEHLIDMDHEASFGAFLVG 281

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 1465611

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Post-processing: Minimum Match 0%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1478	100.0	281	10	US-09-919-039-118
7	1478	100.0	281	13	US-10-011-125-4
8	1478	100.0	281	13	US-10-001-054-54
9	1478	100.0	281	14	US-10-093-766-54
10	1478	100.0	281	14	US-10-174-654-11
11	1478	100.0	281	14	US-10-151-882-41
12	1478	100.0	281	14	US-10-218-547-20
13	1478	100.0	281	14	US-10-322-673-72

14	1478	100.0	281	14	US-10-139-785-66	Sequence 66, Appl
15	1478	100.0	281	14	US-10-310-793-26	Sequence 26, Appl
16	1478	100.0	281	15	US-10-279-687-8	Sequence 8, Appl
17	1478	100.0	281	15	US-10-292-486-5	Sequence 5, Appl
18	1478	100.0	281	15	US-10-333-712-1	Sequence 1, Appl
19	1478	100.0	281	15	US-10-662-429-2	Sequence 2, Appl
20	1478	100.0	281	15	US-10-202-062-20	Sequence 20, Appl
21	1478	100.0	281	15	US-10-662-431-2	Sequence 2, Appl
22	1478	100.0	281	15	US-10-662-430-2	Sequence 2, Appl
23	1478	100.0	281	15	US-10-652-244-2	Sequence 2, Appl
24	1478	100.0	281	16	US-10-381-160-5	Sequence 5, Appl
25	1478	100.0	281	16	US-10-755-889-210	Sequence 210, App
26	1478	100.0	281	16	US-10-491-326-1	Sequence 1, Appl
27	1478	100.0	281	17	US-10-771-254-1	Sequence 1, Appl
28	1478	100.0	281	17	US-10-855-559-2	Sequence 2, Appl
29	1478	100.0	281	17	US-10-451-200-5	Sequence 5, Appl
30	1478	100.0	281	17	US-10-495-353-1	Sequence 1, Appl
31	1478	100.0	281	17	US-10-652-979-1	Sequence 1, Appl
32	1469	99.4	279	13	US-10-066-209-3	Sequence 3, Appl
33	1456	98.5	279	16	US-10-367-094-22	Sequence 22, Appl
34	1437	97.2	283	17	US-10-978-203-23	Sequence 23, Appl
35	1269.5	85.9	246	9	US-09-855-544A-13	Sequence 13, Appl
36	1017	68.8	208	9	US-09-855-544A-16	Sequence 16, Appl
37	988	66.8	253	15	US-10-652-244-11	Sequence 11, Appl
38	988	66.8	256	15	US-10-652-244-13	Sequence 13, Appl
39	985.5	66.7	461	15	US-10-389-223A-6	Sequence 6, Appl
40	982	66.4	480	15	US-10-389-223A-4	Sequence 4, Appl
41	978	66.2	614	15	US-10-389-223A-2	Sequence 2, Appl
42	964.5	65.3	296	14	US-10-185-425-5	Sequence 5, Appl
43	937.5	63.4	188	9	US-09-855-544A-14	Sequence 14, Appl
44	930	62.9	291	10	US-09-873-829-6	Sequence 6, Appl
45	930	62.9	291	13	US-10-017-910-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1  
US-08-916-625B-6  
; Sequence 6, Application US/08916625B  
; Publication No. US20010010924A1  
; GENERAL INFORMATION:  
; APPLICANT: DEEN, KEITH C.  
; APPLICANT: YOUNG, PETER R.  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED  
; TITLE OF INVENTION: RECEPTOR, TR6  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/916,625B  
; FILING DATE: 22-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/853,684  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: 60/041,230  
; FILING DATE: 14-MARCH-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-50008-1  
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-916-625B-6

Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTQCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60
Db 1 MAMMEVGGPSLGGTQCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60

Qy 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNIISPLVREGRGP 120
Db 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNIISPLVREGRGP 120

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSPDPILLMKSARNCSCKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSPDPILLMKSARNCSCKDAEYGLY 240

Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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## RESULT 2

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US-08-971-317A-8
; Sequence 8, Application US/08971317A
; Publication No. US20010010925A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,317A
; FILING DATE: 17-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goller, Mimi C
; REGISTRATION NUMBER: 39, 046
; REFERENCE/DOCKET NUMBER: 6255.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 935-7550
; TELEFAX: (847) 938-2623
; TELEX:
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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20010010925A1e
; US-08-971-317A-8
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Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTQCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60
Db 1 MAMMEVGGPSLGGTQCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60

Qy 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNIISPLVREGRGP 120
Db 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNIISPLVREGRGP 120

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSPDPILLMKSARNCSCKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSPDPILLMKSARNCSCKDAEYGLY 240

Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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## RESULT 3

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US-09-813-329-17
; Sequence 17, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-813-329-17
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Query Match 100.0%; Score 1478; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTQCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60
Db 1 MAMMEVGGPSLGGTQCVLIIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGGIACFLKE 60

Qy 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNIISPLVREGRGP 120
Db 61 DDSYWDPNDESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNIISPLVREGRGP 120

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSPDPILLMKSARNCSCKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSPDPILLMKSARNCSCKDAEYGLY 240
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Db 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNSCWSDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 4  
US-09-193-663-8  
; Sequence 8, Application US/09193663  
; Patent No. US200200556241  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF  
; FILE REFERENCE: 6255.US.02  
; CURRENT APPLICATION NUMBER: US/09/193,663  
; CURRENT FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: 60/065,916  
; EARLIER FILING DATE: 1997-11-17  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-193-663-8

Query Match 100.0%; Score 1478; DB 9; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANMEVQGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60  
Db 1 MANMEVQGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DSYWDPNDESNMSPCWQVKQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DSYWDPNDESNMSPCWQVKQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGQ 120

QY 121 RAAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180  
Db 121 RAAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180

QY 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNSCWSDAEYGLY 240  
Db 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 5  
US-09-934-465-1  
; Sequence 1, Application US/09934465  
; Patent No. US20020102233A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: APO-2 LIGAND  
; FILE REFERENCE: 11669.22US03  
; CURRENT APPLICATION NUMBER: US/09/934,465  
; CURRENT FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: 08/584,031  
; PRIOR FILING DATE: 1996-01-09  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-934-465-1

Query Match 100.0%; Score 1478; DB 9; Length 281;

Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANMEVQGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60  
Db 1 MANMEVQGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DSYWDPNDESNMSPCWQVKQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DSYWDPNDESNMSPCWQVKQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGQ 120

QY 121 RAAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180  
Db 121 RAAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180

QY 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNSCWSDAEYGLY 240  
Db 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 6  
US-09-919-039-118  
; Sequence 118, Application US/09919039  
; Publication No. US20030108871A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES  
; FILE REFERENCE: PA-0035 US  
; CURRENT APPLICATION NUMBER: US/09/919,039  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/222,113  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 401  
; SOFTWARE: PERL Program  
; SEQ ID NO 118  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1  
US-09-919-039-118

Query Match 100.0%; Score 1478; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANMEVQGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60  
Db 1 MANMEVQGGPSLGTCLVIFVTLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DSYWDPNDESNMSPCWQVKQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DSYWDPNDESNMSPCWQVKQLRQLVRKWLRTSEETISTVQEKQONISPLVRERGQ 120

QY 121 RAAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180  
Db 121 RAAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180

QY 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNSCWSDAEYGLY 240  
Db 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7

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US-10-011-125-4
; Sequence 4, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-011-125-4

Query Match          100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVQGPGLGQTCVLIVITFTVLLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MAMVEVQGPGLGQTCVLIVITFTVLLQSLCVAVTYYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDESMNSPCQVQWQLRQLVRYKMLILRTSEETISTVQKQKQNISPLVRERGPQ 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 DDSYWDPNDESMNSPCQVQWQLRQLVRYKMLILRTSEETISTVQKQKQNISPLVRERGPQ 120

QY 121 RVAAHITGTRGNTLSSPNSKNEALGRKINKNSWESSRSGHSFLSNLHRLNGELVIEHKG 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 RVAAHITGTRGNTLSSPNSKNEALGRKINKNSWESSRSGHSFLSNLHRLNGELVIEHKG 180

QY 181 FYIYSQTYFRQBEIKENTKNDKQVYIYKITSYDPDILLMKSRNSCWSKDAEYGLY 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 FYIYSQTYFRQBEIKENTKNDKQVYIYKITSYDPDILLMKSRNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKNDRIFVSVTNEHLIDMDHEASFGAFLVG 281
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 SIYQGGIFELKNDRIFVSVTNEHLIDMDHEASFGAFLVG 281

RESULT 8
US-10-001-054-54
; Sequence 54, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona
; APPLICANT: Shelton, David
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE REFERENCE: P3034R1PCT
; CURRENT APPLICATION NUMBER: US/10/001,054
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/096891
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/096894
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100263
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/107783
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112420
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/115554
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116533
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/131294
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/187202
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/209832
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/180997
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: 09/218517
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 09/284291
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380913
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 09/403297
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/423741
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 09/709238
; PRIOR FILING DATE: 2000-11-08
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; PRIOR APPLICATION NUMBER: 09/803706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 09/866034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/872035
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/882636
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/924419
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/927796
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/941992
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: PCT/US98/18824
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US99/00106
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/08615
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28634
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00376
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/06884
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/13705
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/14941
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/22031
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678

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; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US01/27099
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-54

Query Match      100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MANMEVGGPSLGGTCTVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSGIACFLKE 60
Db      1  MANMEVGGPSLGGTCTVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSGIACFLKE 60

Qy      61  DDSYWDNDDEESMNSPCWQVQWQLRQLVRKMLRTSETISTVQEKQONISPLVREGPQ 120
Db      61  DDSYWDNDDEESMNSPCWQVQWQLRQLVRKMLRTSETISTVQEKQONISPLVREGPQ 120

Qy      121  RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
Db      121  RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

Qy      181  FYYISQTYFRFQEEIKENTKNDKQVQYIKYTSYDPPILLMKSAKNSCKDAEYGLY 240
Db      181  FYYISQTYFRFQEEIKENTKNDKQVQYIKYTSYDPPILLMKSAKNSCKDAEYGLY 240

Qy      241  SIYQGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAFLVG 281
Db      241  SIYQGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 9
US-10-093-766-54
; Sequence 54, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Jones, David A.
; APPLICANT: Lasek, Amy W.
; APPLICANT: Karpf, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093,766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
US-10-093-766-54

Query Match      100.0%; Score 1478; DB 14; Length 281;

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Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60  
Db |||||  
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60  
Db |||||

Qy 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQSKQNI SPLVRGPQ 120  
Db |||||

Qy 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQSKQNI SPLVRGPQ 120  
Db |||||

Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Db |||||

Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Db |||||

Qy 181 FYIYSQTYFRPQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSKDAEYGLY 240  
Db |||||

Qy 181 FYIYSQTYFRPQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSKDAEYGLY 240  
Db |||||

Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db |||||

Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db |||||

RESULT 10  
US-10-174-654-11  
; Sequence 11, Application US/10174654  
; Publication No. US20030044937A1  
; GENERAL INFORMATION:  
; APPLICANT: Bienkowski, Michael J  
; Jones, Cynthia J  
; TITLE OF INVENTION: TNF-Related Death Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property  
; Legal Services  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 19-Jun-2002  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerber, Lori L.  
; REGISTRATION NUMBER: 41,113  
; REFERENCE/DOCKET NUMBER: 6111.N CNI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616/833-0974  
; TELEFAX: 616/833-8897  
; TELETYPE: 224401  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-174-654-11

Query Match 100.0%; Score 1478; DB 14; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60  
Db |||||

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60  
Db |||||

Qy 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQSKQNI SPLVRGPQ 120  
Db |||||

Qy 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQSKQNI SPLVRGPQ 120  
Db |||||

Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Db |||||

Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Db |||||

Qy 181 FYIYSQTYFRPQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSKDAEYGLY 240  
Db |||||

Qy 181 FYIYSQTYFRPQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSKDAEYGLY 240  
Db |||||

Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db |||||

Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db |||||

RESULT 11  
US-10-151-882-41  
; Sequence 41, Application US/10151882  
; Publication No. US20030059862A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)  
; FILE REFERENCE: PF554  
; CURRENT APPLICATION NUMBER: US/10/151,882  
; PRIOR FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: 60/293,100  
; PRIOR FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 41  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-151-882-41

Query Match 100.0%; Score 1478; DB 14; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60  
Db |||||

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60  
Db |||||

Qy 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQSKQNI SPLVRGPQ 120  
Db |||||

Qy 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQSKQNI SPLVRGPQ 120  
Db |||||

Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Db |||||

Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Db |||||

Qy 181 FYIYSQTYFRPQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSKDAEYGLY 240  
Db |||||

Qy 181 FYIYSQTYFRPQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSKDAEYGLY 240  
Db |||||

Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db |||||

Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db |||||

RESULT 12  
US-10-218-547-20  
; Sequence 20, Application US/10218547  
; Publication No. US20030100074A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel

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; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-10-218-547-20

Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGTCTVLIVFTVLLQSLCAVAVTVYFTNKLQMDQKYSKGIACFLKE 60
Db 1 MAMMEVGGPSLGTCTVLIVFTVLLQSLCAVAVTVYFTNKLQMDQKYSKGIACFLKE 60

Qy 61 DDSYWDNDDESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERG 120
Db 61 DDSYWDNDDESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERG 120

Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180

Qy 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWCKDAEYGLY 240

Qy 241 SIYGGGIFELKENDRIEFSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYGGGIFELKENDRIEFSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 13
US-10-322-673-72
; Sequence 72, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-322-673-72

Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGTCTVLIVFTVLLQSLCAVAVTVYFTNKLQMDQKYSKGIACFLKE 60
Db 1 MAMMEVGGPSLGTCTVLIVFTVLLQSLCAVAVTVYFTNKLQMDQKYSKGIACFLKE 60

Qy 61 DDSYWDNDDESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERG 120
Db 61 DDSYWDNDDESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERG 120

Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180

Qy 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWCKDAEYGLY 240

Qy 241 SIYGGGIFELKENDRIEFSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYGGGIFELKENDRIEFSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14
US-10-139-785-66
; Sequence 66, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-139-785-66

Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGTCTVLIVFTVLLQSLCAVAVTVYFTNKLQMDQKYSKGIACFLKE 60
Db 1 MAMMEVGGPSLGTCTVLIVFTVLLQSLCAVAVTVYFTNKLQMDQKYSKGIACFLKE 60

Qy 61 DDSYWDNDDESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERG 120
Db 61 DDSYWDNDDESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERG 120

Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
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Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVHKG 180
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKARSNCWKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKARSNCWKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 15
US-10-793-793-26
; Sequence 26, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-310-793-26

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGTGTCVLIVFTVLLQSLCAVAVTVVFTNELKOMQDKYKSGIACFLKE 60
Db 1 MAMMEVGGPSLGTGTCVLIVFTVLLQSLCAVAVTVVFTNELKOMQDKYKSGIACFLKE 60

Qy 61 DDSYWDPNDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQNI SPLVRERGPQ 120
Db 61 DDSYWDPNDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQNI SPLVRERGPQ 120

Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVHKG 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVHKG 180

Qy 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKARSNCWKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKARSNCWKDAEYGLY 240

RESULT 16
US-10-279-687-8
; Sequence 8, Application US/10279687
; Publication No. US20030211509A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255.US.C2
; CURRENT APPLICATION NUMBER: US/10/279,687
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 10/105,738
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/193,663
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/065,916
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-687-8

Query Match 100.0%; Score 1478; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGTGTCVLIVFTVLLQSLCAVAVTVVFTNELKOMQDKYKSGIACFLKE 60
Db 1 MAMMEVGGPSLGTGTCVLIVFTVLLQSLCAVAVTVVFTNELKOMQDKYKSGIACFLKE 60

Qy 61 DDSYWDPNDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQNI SPLVRERGPQ 120
Db 61 DDSYWDPNDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQNI SPLVRERGPQ 120

Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVHKG 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVHKG 180

Qy 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKARSNCWKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKARSNCWKDAEYGLY 240

RESULT 17
US-10-292-486-5
; Sequence 5, Application US/10292486
; Publication No. US20030228309A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors
; FILE REFERENCE: PF532P1
; CURRENT APPLICATION NUMBER: US/10/292,486
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/403,376
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/377,973
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/331,309
```

```
Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKARSNCWKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 16
US-10-279-687-8
; Sequence 8, Application US/10279687
; Publication No. US20030211509A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255.US.C2
; CURRENT APPLICATION NUMBER: US/10/279,687
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 10/105,738
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/193,663
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/065,916
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-687-8

Query Match 100.0%; Score 1478; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGTGTCVLIVFTVLLQSLCAVAVTVVFTNELKOMQDKYKSGIACFLKE 60
Db 1 MAMMEVGGPSLGTGTCVLIVFTVLLQSLCAVAVTVVFTNELKOMQDKYKSGIACFLKE 60

Qy 61 DDSYWDPNDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQNI SPLVRERGPQ 120
Db 61 DDSYWDPNDESMNSPCQVQKWLQRLVRKMLRTSEETISTVQEKQNI SPLVRERGPQ 120

Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVHKG 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVHKG 180

Qy 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKARSNCWKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKARSNCWKDAEYGLY 240

RESULT 17
US-10-292-486-5
; Sequence 5, Application US/10292486
; Publication No. US20030228309A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors
; FILE REFERENCE: PF532P1
; CURRENT APPLICATION NUMBER: US/10/292,486
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/403,376
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/377,973
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/331,309
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; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/986,149
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,359
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/295,018
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/252,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/248,847
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/246,612
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-292-486-5

Query Match
Best Local Similarity 100.0%; Score 1478; DB 15; Length 281;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; 1 MAMMEVGGPSLGTQCVLIIVFTVLLQSLCAVAVTVYVFTNKLKQMDKYKSGIACFLKE 60
; 1 MAMMEVGGPSLGTQCVLIIVFTVLLQSLCAVAVTVYVFTNKLKQMDKYKSGIACFLKE 60
; 61 DDSYWDNDRESMNSPCWQVQWQLRQLVRKMLTSETISTVQEKQONISPLVREGPQ 120
; 61 DDSYWDNDRESMNSPCWQVQWQLRQLVRKMLTSETISTVQEKQONISPLVREGPQ 120
; 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
; 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
; 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSKSKDAEYGLY 240
; 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSKSKDAEYGLY 240
; 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
; 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 19
US-10-662-429-2
; Sequence 2, Application US/10662429
; Publication No. US2004009347A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,429
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-10-662-429-2

Query Match
Best Local Similarity 100.0%; Score 1478; DB 15; Length 281;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; 1 MAMMEVGGPSLGTQCVLIIVFTVLLQSLCAVAVTVYVFTNKLKQMDKYKSGIACFLKE 60
; 1 MAMMEVGGPSLGTQCVLIIVFTVLLQSLCAVAVTVYVFTNKLKQMDKYKSGIACFLKE 60
; 61 DDSYWDNDRESMNSPCWQVQWQLRQLVRKMLTSETISTVQEKQONISPLVREGPQ 120
; 61 DDSYWDNDRESMNSPCWQVQWQLRQLVRKMLTSETISTVQEKQONISPLVREGPQ 120
; 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
; 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
; 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSKSKDAEYGLY 240
; 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSKSKDAEYGLY 240
; 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
; 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 18
US-10-333-712-1
; Sequence 1, Application US/10333712
; Publication No. US2004005314A1
; GENERAL INFORMATION:
; APPLICANT: Escandon, Enrique
; APPLICANT: Fox, Judith A.
; APPLICANT: Kelley, Sean K.
; APPLICANT: Xiang, Hong
; TITLE OF INVENTION: APO-2L RECEPTOR AGONIST AND CPT-11 SYNERGISM
; FILE REFERENCE: P1839R1
; CURRENT APPLICATION NUMBER: US/10/333,712
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: PCT/US01/23691
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,256
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-333-712-1

Query Match
Best Local Similarity 100.0%; Score 1478; DB 15; Length 281;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGPQ 120  
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQKVQYIYKTSYDPDILLMKSARNCSKDAEYGLY 240  
Db 181 FYIYSQTYFRFQBEIKENTKNDKQKVQYIYKTSYDPDILLMKSARNCSKDAEYGLY 240  
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

## RESULT 20

US-10-202-062-20  
; Sequence 20, Application US/10202062  
; Publication No. US20040038349A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.,  
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members  
; FILE REFERENCE: PF559  
; CURRENT APPLICATION NUMBER: US/10/202,062  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 60/307,838  
; PRIOR FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 20  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: human  
US-10-202-062-20

Query Match 100.0%; Score 1478; DB 15; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAMMEVQGGPSLGTQCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGTQCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60  
Qy 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGPQ 120  
Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGPQ 120  
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQKVQYIYKTSYDPDILLMKSARNCSKDAEYGLY 240  
Db 181 FYIYSQTYFRFQBEIKENTKNDKQKVQYIYKTSYDPDILLMKSARNCSKDAEYGLY 240  
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

## RESULT 21

US-10-662-431-2  
; Sequence 21, Application US/10662431  
; Publication No. US20040047864A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben, Steven M  
; TITLE OF INVENTION: Apoptosis Inducing Molecule I  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville

; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/662,431  
; FILING DATE: 16-Sep-2003  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/816,981  
; FILING DATE: 13-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kimball, Paul, C.  
; REGISTRATION NUMBER: 34,610  
; REFERENCE/DOCKET NUMBER: PF261  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-662-431-2

Query Match 100.0%; Score 1478; DB 15; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.3e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAMMEVQGGPSLGTQCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGTQCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60  
Qy 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGPQ 120  
Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGPQ 120  
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQKVQYIYKTSYDPDILLMKSARNCSKDAEYGLY 240  
Db 181 FYIYSQTYFRFQBEIKENTKNDKQKVQYIYKTSYDPDILLMKSARNCSKDAEYGLY 240  
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

## RESULT 22

US-10-662-430-2  
; Sequence 22, Application US/10662430  
; Publication No. US20040048340A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben, Steven M  
; TITLE OF INVENTION: Apoptosis Inducing Molecule I  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,430
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-662-430-2

Query Match 100.0%; Score 1478; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCLVIVFTVLLQSLCAVAVTVYFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGTCLVIVFTVLLQSLCAVAVTVYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDNDDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERG 120
DB 61 DDSYWDNDDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERG 120

QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHG 180
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHG 180

QY 181 FYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
DB 181 FYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 24
US-10-381-160-5
; Sequence 5, Application US/10381160
; Publication No. US20040131587A1
; GENERAL INFORMATION:
; APPLICANT: IMMUNEX CORPORATION
; TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING COMBINATION THERAPY
; FILE REFERENCE: 2993-WO
; CURRENT APPLICATION NUMBER: US/10/381,160
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/242,868
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-381-160-5

Query Match 100.0%; Score 1478; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCLVIVFTVLLQSLCAVAVTVYFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGTCLVIVFTVLLQSLCAVAVTVYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDNDDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERG 120
DB 61 DDSYWDNDDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERG 120

QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHG 180
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHG 180

QY 181 FYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240
DB 181 FYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

US-10-652-244-2
; Sequence 2, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
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Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 25
US-10-755-889-210
; Sequence 210, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 210
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-210

Query Match 100.0%; Score 1478; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGKIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGKIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 26
US-10-491-326-1
; Sequence 1, Application US/10491326
; Publication No. US20040186051A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: Robert F. Kelley, Stephanie H. Lindstrom
; TITLE OF INVENTION: APO-2 Ligand Variants and Uses Thereof
; FILE REFERENCE: P1858R1
; CURRENT APPLICATION NUMBER: US/10/491,326
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US 60/326,622
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT

Query Match 100.0%; Score 1478; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGKIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGKIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 27
US-10-771-254-1
; Sequence 1, Application US/10771254
; Publication No. US20050020498A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: Flores, Heather
; APPLICANT: Lin, Tanva P.
; APPLICANT: Pai, Roger
; APPLICANT: Shanrokh, Zahra
; APPLICANT: Matthews, Timothy C.
; TITLE OF INVENTION: APO-2 LIGAND/TRAIL FORMULATIONS
; FILE REFERENCE: P1857R1P1
; CURRENT APPLICATION NUMBER: US/10/771,254
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/338,249
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: PCT/US02/36251
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-254-1

Query Match 100.0%; Score 1478; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGKIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGKIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240
```

```
; ORGANISM: Homo Sapiens
US-10-491-326-1

Query Match 100.0%; Score 1478; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGKIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGKIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 27
US-10-771-254-1
; Sequence 1, Application US/10771254
; Publication No. US20050020498A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: Flores, Heather
; APPLICANT: Lin, Tanva P.
; APPLICANT: Pai, Roger
; APPLICANT: Shanrokh, Zahra
; APPLICANT: Matthews, Timothy C.
; TITLE OF INVENTION: APO-2 LIGAND/TRAIL FORMULATIONS
; FILE REFERENCE: P1857R1P1
; CURRENT APPLICATION NUMBER: US/10/771,254
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/338,249
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: PCT/US02/36251
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-254-1

Query Match 100.0%; Score 1478; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGKIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGKIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQVYIYKTSYPPDPILLMKARNCSWCKDAEYGLY 240
```

```

; ORGANISM: Homo sapiens
US-10-451-200-5

Query Match      100.0%; Score 1478; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 MAMMEVOGGSLSGTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVOGGSLSGTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Qy 61 DDSYWDNDDESNNSPCWQVKWQLROLVRKWLILRTSEETISTVQEKQNTSPLVRERGQ 120
Db 61 DDSYWDNDDESNNSPCWQVKWQLROLVRKWLILRTSEETISTVQEKQNTSPLVRERGQ 120

Qy 121 RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVITHEKG 180
Db 121 RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVITHEKG 180

Qy 181 FYYIYSQTYFRFOBEIKENTKNDQMVOYIYKYTSPDPTILLMKASRNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFOBEIKENTKNDQMVOYIYKYTSPDPTILLMKASRNSCWSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 30
US-10-495-353-1
; Sequence 1, Application US/10495353
; Publication No. US20050080006A1
; GENERAL INFORMATION:
; APPLICANT: FLORES, Heather
; APPLICANT: LIN, Tanya P.
; APPLICANT: PAI, Roger
; APPLICANT: SHAHROKH, Zahra
; APPLICANT: MATTHEWS, Timothy
; TITLE OF INVENTION: Apo-2 LIGAND/TRAIL FORMULATIONS
; FILE REFERENCE: P1857R1
; CURRENT APPLICATION NUMBER: US/10/495,353
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: PCT/US02/36251
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/338,249
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-495-353-1

Query Match      100.0%; Score 1478; DB 17; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVOGGSLSGTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVOGGSLSGTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Qy 61 DDSYWDNDDESNNSPCWQVKWQLROLVRKWLILRTSEETISTVQEKQNTSPLVRERGQ 120
Db 61 DDSYWDNDDESNNSPCWQVKWQLROLVRKWLILRTSEETISTVQEKQNTSPLVRERGQ 120

Qy 121 RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVITHEKG 180
Db 121 RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVITHEKG 180

Qy 181 FYYIYSQTYFRFOBEIKENTKNDQMVOYIYKYTSPDPTILLMKASRNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFOBEIKENTKNDQMVOYIYKYTSPDPTILLMKASRNSCWSKDAEYGLY 240

```

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 |||||  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 |||||

RESULT 31

US-10-652-979-1  
 ; Sequence 1, Application US/10652979  
 ; Publication No. US20050089958A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; TITLE OF INVENTION: Apo-2 Ligand  
 ; FILE REFERENCE: P097823C1  
 ; CURRENT APPLICATION NUMBER: US/10/652,979  
 ; PRIORITY FILING DATE: 2003-08-29  
 ; PRIOR APPLICATION NUMBER: US 09/060,533  
 ; PRIORITY FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: US 09/007,886  
 ; PRIORITY FILING DATE: 1998-01-15  
 ; PRIOR APPLICATION NUMBER: US 08/780,496  
 ; PRIORITY FILING DATE: 1997-01-08  
 ; PRIOR APPLICATION NUMBER: US 60/009,755  
 ; PRIORITY FILING DATE: 1996-01-09  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SEQ ID NO 1  
 ; LENGTH: 281  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-652-979-1

Query Match 100.0%; Score 1478; DB 17; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-128; Indels 0; Gaps 0;  
 Matches 281; Conservative 0; Mismatches 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVFTNKLQMDKYSGIACFLKE 60  
 |||||  
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVFTNKLQMDKYSGIACFLKE 60  
 |||||  
 QY 61 DSDYNDPDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPGQ 120  
 |||||  
 DB 61 DSDYNDPDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPGQ 120  
 |||||  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 |||||  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 |||||  
 QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSKDAEYGLY 240  
 |||||  
 DB 181 FYIYSQTYFRFQBEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSKDAEYGLY 240  
 |||||  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 |||||  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 |||||

RESULT 32

US-10-066-209-3  
 ; Sequence 3, Application US/10066209  
 ; Publication No. US20020115110A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brigham-Burke, Michael R.  
 ; APPLICANT: Young, Peter R.  
 ; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND  
 ; FILE REFERENCE: GH-50030-D1  
 ; CURRENT APPLICATION NUMBER: US/10/066,209  
 ; PRIORITY FILING DATE: 2001-10-25  
 ; PRIOR APPLICATION NUMBER: 09/072,993  
 ; PRIORITY FILING DATE: 1998-05-06  
 ; PRIOR APPLICATION NUMBER: 60/055,513  
 ; PRIORITY FILING DATE: 1997-08-13  
 ; PRIOR APPLICATION NUMBER: 60/056,980

; PRIOR FILING DATE: 1997-08-26  
 ; PRIOR APPLICATION NUMBER: 60/057,550  
 ; PRIOR FILING DATE: 1997-08-29  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 279  
 ; TYPE: PRT  
 ; ORGANISM: HOMO SAPIENS  
 US-10-066-209-3  
 Query Match 99.4%; Score 1469; DB 13; Length 279;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-128;  
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 MMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVFTNKLQMDKYSGIACFLKEDD 62  
 |||||  
 DB 1 MMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVFTNKLQMDKYSGIACFLKEDD 60  
 |||||  
 QY 63 SYNDPDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPGQV 122  
 |||||  
 DB 61 SYNDPDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPGQV 120  
 |||||  
 QY 123 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKGFY 182  
 |||||  
 DB 121 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKGFY 180  
 |||||  
 QY 183 YIYSQTYFRFQBEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSKDAEYGLYSI 242  
 |||||  
 DB 181 YIYSQTYFRFQBEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSKDAEYGLYSI 240  
 |||||  
 QY 243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 |||||  
 DB 241 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279  
 |||||

RESULT 33

US-10-367-094-22  
 ; Sequence 22, Application US/10367094  
 ; Publication No. US20040170982A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: David W. Morris  
 ; APPLICANT: Marc Malandro  
 ; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer  
 ; FILE REFERENCE: 529452001500  
 ; CURRENT APPLICATION NUMBER: US/10/367,094  
 ; PRIORITY FILING DATE: 2003-02-14  
 ; NUMBER OF SEQ ID NOS: 203  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 22  
 ; LENGTH: 279  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-367-094-22

Query Match 98.5%; Score 1456; DB 16; Length 279;  
 Best Local Similarity 99.3%; Pred. No. 1.4e-126;  
 Matches 279; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVFTNKLQMDKYSGIACFLKE 60  
 |||||  
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVFTNKLQMDKYSGIACFLKE 60  
 |||||  
 QY 61 DSDYNDPDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPGQ 120  
 |||||  
 DB 61 DSDYNDPDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPGQ 120  
 |||||  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 |||||  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 |||||  
 QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQIYKYTSYPPDILLMKSARNCSKDAEYGLY 240  
 |||||

Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYG-- 238

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
|||||

Db 239 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279  
|||||

RESULT 34  
US-10-978-203-23  
; Sequence 23, Application US/10978203  
; Publication No. US20050112666A1  
; GENERAL INFORMATION:  
; APPLICANT: Chicheportiche, Yves  
; APPLICANT: Browning, Jeffrey  
; TITLE OF INVENTION: Tumor Necrosis Factor Related Ligand  
; FILE REFERENCE: A003  
; CURRENT APPLICATION NUMBER: US/10/978,203  
; CURRENT FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: 60/023,541  
; PRIOR FILING DATE: 1996-08-07  
; PRIOR APPLICATION NUMBER: 60/028,515  
; PRIOR FILING DATE: 1996-10-18  
; PRIOR APPLICATION NUMBER: 60/040,820  
; PRIOR FILING DATE: 1997-03-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 283  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-10-978-203-23

Query Match 97.2%; Score 1437; DB 17; Length 283;  
Best Local Similarity 97.5%; Pred. No. 8.1e-125;  
Matches 278; Conservative 0; Mismatches 1; Indels 6; Gaps 2;

Qy 1 MAMMEVQGGPSLGQTCVLIIVFTVLLQSLCVAVTVYVFTNELKQMDKYKSGIACFLKE 60  
|||||

Db 1 MAMMEVQGGPSLGQTCVLIIVFTVLLQSLCVAVTVYVFTNELKQMDKYKSGIACFLKE 60  
|||||

Qy 61 DDSYWDNDDESMNSPC-----WQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRE 116  
|||||

Db 61 DDSYWDNDDESMNSPCQWKQWKQQLRQLVRKMLRTSEETISTVQEKQONISPLVRE 120  
|||||

Qy 117 RGPORVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVI 176  
|||||

Db 121 RGPORVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVI 180  
|||||

Qy 177 HEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAE 236  
|||||

Db 181 HEKGFYIYSQTYFRFQBEIKENTKNDKQMVVYIYKYTSYDPDPILLMKSARNSCWSKDAE 240  
|||||

Qy 237 YGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
|||||

Db 241 YG--SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 283  
|||

Search completed: June 3, 2005, 12:06:54  
Job time : 56 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2005, 06:26:36 ; Search time 174 Seconds  
(without alignments)  
715.145 Million cell updates/sec

Title: US-10-662-431-2\_COPY\_39\_281

Perfect score: 1287  
Sequence: 1 TNELKQMDKYSGIACFL.....NEHLIDMDHEASFFGAFVIG 243

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 804456

Minimum DB seq length: 0  
Maximum DB seq length: 243

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	305.5	23.7	214	2 Q9DDZ5	Q9ddz5 brachydanio
2	291	22.6	63	2 Q6JSD9	Q6jds9 homo sapien
3	175.5	13.6	169	2 Q9WV90	Q9wv90 marmota mon
4	163.5	12.7	131	2 Q6J3Q6	Q6j3q6 canis famil
5	160	12.4	174	1 TN15_HUMAN	O95150 homo sapien
6	159.5	12.4	240	1 TN14_HUMAN	O43557 homo sapien
7	157	12.2	154	2 Q8MJ19	Q8mj19 macaca mula
8	152.5	11.8	239	1 TN14_MOUSE	Q9gyh9 mus musculus
9	151.5	11.8	227	2 Q7T2Q3	Q7t2q3 cyprinus ca
10	144.5	11.2	216	2 Q70332	O70332 mesocricetu
11	143	11.1	241	2 Q6U817	Q6u817 lateolabrax
12	141	11.0	231	2 Q8AW02	Q8aw02 cyprinus ca
13	137.5	10.7	232	2 Q8OX44	Q8ox44 peromyscus
14	137.5	10.7	234	2 Q7T9C7	Q7t9c7 brachydanio
15	136.5	10.6	235	1 TNFA_RABIT	P04924 oryctolagus
16	135	10.5	156	2 Q91ZL4	Q91z14 sigmodon hi
17	135	10.5	215	2 Q9BEE8	Q9bee8 erinaceus e
18	135	10.5	217	2 Q9BER6	Q9ber6 peromyscus
19	134.5	10.5	204	1 TNFB_FIG	P28445 sus scrofa
20	132.5	10.3	234	1 TNFA_CAVPO	P51435 cavia porce
21	130.5	10.1	222	2 Q7T1U4	Q7t1u4 pagrus majo
22	130	10.1	232	1 TNFA_PIG	P23563 sus scrofa
23	129.5	10.1	235	1 TNFA_PERLE	P36939 peromyscus
24	128	9.9	230	2 Q8JG37	Q8jg37 ictalurus p
25	127.5	9.9	204	1 TNFB_BOVIN	Q06600 bos taurus
26	126.5	9.8	225	2 Q9IB42	Q9ib42 paralichthy
27	126	9.8	234	1 TNFA_HORSE	P29553 equus cabal
28	125	9.7	215	2 Q99ND1	Q99nd1 sciurus vul
29	125	9.7	233	1 TNFA_MARMO	O35734 marmota mon
30	124	9.6	216	2 Q9BEC4	Q9bec4 talpa europ
31	123.5	9.6	216	2 Q9BEC9	Q9bec9 ochotona pr

ALIGNMENTS

RESULT 1

Q9DDZ5 PRELIMINARY; PRT; 214 AA.

AC Q9DDZ5;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE TRAIL-like protein.

GN Name=tnfsf101;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Boe J., Goetz F.W.;  
RT "Molecular cloning and expression of a TNF receptor and two TNF  
ligands in the fish ovary.";  
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481 (2001).  
DR EMBL; AF250041; AAG47640.1;  
DR HSSP; P50591; 1D2Q.  
DR ZFIN; ZDB-GENE-010801-1; tnfsf101.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005184; F:tumor necrosis factor receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR006052; TNF family.  
DR InterPro; IPR008983; TNF-like.  
DR InterPro; IPR003636; TNF\_subf.  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;

Query Match 23.7%; Score 305.5; DB 2; Length 214;  
Best Local Similarity 37.6%; Pred. No. 4.4e-17;  
Matches 62; Conservative 37; Mismatches 59; Indels 7; Gaps 3;

QY 82 QVAAHTIGTRGRNT-----LSPNSKNEALGRKINSWESSRSGH3FLSNLHRLNGEL 136

Db 47 QPRAHLTLSSASDNRSPQSDMHQPFDLHSCRPVHTW-ANKSFGAHLNMTLTNGEL 105

QY 137 VTHEKGFYIYSQTYFRF-QBEIKENTKNDQMYYIYKYTSYDPDILLMKSRNSWSK 195

Db 106 RVPQDGRYLYSQVYFRYPSPSDSQSSVSHQLVQCIYKTSYLNPIQLLKGVTGKCAP 165

QY 196 DAETGLVSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240

Db 166 DAETALSHVYQGLFELRAGDEVFVSPTMTVYGEDSSSYFGAF 210

RESULT 2

Q6JSD9

Query Match	12.7%	Score 163.5;	DB 2;	Length 131;
Best Local Similarity	27.1%;	Pred. No. 1.1e-05;		
Matches 42; Conservative	33;	Mismatches 48;	Indels 33;	Gaps 7;
Qy	93	GRSNTLSSPNRQNEKALGRINKINSWESSRSRGHSFLSNILHRLNGELVIEHKGFYIYSQTFF	152	
Db	1	KGNRSRIP-----LEWEDT-YGIALVSGVKYKKGGVLINDTGIFYSKYVF	47	

```
QY 153 RFOBEIKENTKNDKQVQYIY-KYTSYDPDILLMK-SARNSC-----WSKDAEYGLYSIY 205
Db 48 RGQ-----SCNNKPLNHKYNRNRSKYFQDLMLMEGKIMNYCTTGQMMWAR-----SSY 94

QY 206 OGGIFELKENDRIFSVSVNEHLMDMDHEASFFGAF 240
Db 95 LGAVNLTADHLYVNVSELSVFSPEESKTFGLY 129

RESULT 5
TN15 HUMAN
ID TN15 HUMAN STANDARD; PRT; 174 AA.
AC O95150;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 15 (Vascular endothelial cell growth inhibitor) (TNF ligand-related molecule 1).
GN Name=TNFSF15; Synonyms=TL1, VEGI;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein;
RX MEDLINE=99091541; PubMed=9972942;
RA Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,
RA Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,
RA Li L.-Y., Gentz R., Yu G.-L.;
RT "VEGI, a novel cytokine of the tumor necrosis factor family, is an
RT angiogenesis inhibitor that suppresses the growth of colon carcinomas
RT in vivo.";
RL FASEB J. 13:181-189(1999).
CC -1- FUNCTION: Inhibits vascular endothelial growth and angiogenesis
CC (in vitro).
CC -1- SUBUNIT: Homotrimer (Potential).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.
CC Detected in placenta, lung, kidney, skeletal muscle, pancreas,
CC spleen, prostate, small intestine and colon.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; AF039390; AAD08783.1; -.
CC HSSP; P50591; 102Q.
CC Genew; HGNC:11931; TNFSF15.
CC MIM; 604052; -.
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005102; F: receptor binding; TAS.
CC GO; GO:0000074; P: regulation of cell cycle; TAS.
CC InterPro; IPR006053; TNF abc.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF-like.
CC Pfam; PF00229; TNF; 1.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01234; TNECROSISFCT.
CC ProDom; PD002012; TNF subf; 1.
CC SMART; SM00207; TNF_1.
CC PROSITE; PS50049; TNF_2; 1.
KW Cycokine; Glycoprotein; Signal-anchor; Transmembrane.
FT DOMAIN 1 12 Cytoplasmic (Potential).
FT TRANSMEM 13 25 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 26 174 Extracellular (Potential).
FT DISULFID 85 125 Potential.
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FT CARBOHYD 56 56 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 152 152 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 174 AA; 20131 MW; CCB83BA7EE673B98 CRC64;

Query Match 12.4%; Score 160; DB 1; Length 174;
Best Local Similarity 35.3%; Pred. No. 3e-05;
Matches 49; Conservative 24; Mismatches 48; Indels 18; Gaps 8;

QY 116 WESSRSGHSFLSN-LHLRNGELVTHKGFYIYISQTYFRFQ-----EIKENTKNDK--QM 168
Db 42 WE-HELGLAFTKRNMYTNKFLIPESGDYFIYSQVTFRGMTSECSERQGRPNKPSI 100

QY 169 VQIYKYT-SYPDPILLMKSNCSWCKDAEYGV---LYSIYOGGIFELKENDRIFSVSTN 224
Db 101 TVVITKVTDSYPTQLLMGTGKVC-----EVGSNWFQPIYLGAMFSLQEGDKLMVNVSD 155

QY 225 EHLIDMDHE-ASFPGAFIV 242
Db 156 ISLVDTYTKEDKTFPGAFLL 174

RESULT 6
TN14 HUMAN
ID TN14 HUMAN STANDARD; PRT; 240 AA.
AC O43557; O75476; Q8WVF8; Q96LD2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry mediator-ligand) (HVEM-L) (UNQ391/PRO726).
GN Name=TNFSF14; Synonyms=HVEM-L, LIGHT;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=9812340; PubMed=9462508; DOI=10.1016/S1074-7613(00)80455-0;
RA Mauri D.N., Ebner R., Montgomery R.I., Kochev K.D., Cheung T.C.,
RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
RA Ware C.F.;
RT "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
RT ligands for herpesvirus entry mediator.";
RL Immunity 8:21-30(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RX TISSUE=Liver;
RX MEDLINE=98438532; PubMed=9765287; DOI=10.1074/jbc.273.42.27548;
RA Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,
RA Tan K.B., Dede K., Spananato J., Silverman C., Hensley P.,
RA DiPrinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
RA Truneh A., Young P.R.;
RA "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for
RA HVEM/TR2, stimulates proliferation of T cells and inhibits HT29 cell
RA growth.";
RL J. Biol. Chem. 273:27548-27556(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
RX MEDLINE=21528948; PubMed=11673523;
RA Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;
RA "Genomic characterization of LIGHT reveals linkage to an immune
RA response locus on chromosome 19p13.3 and distinct isoforms generated
RA by alternate splicing or proteolysis.";
RL J. Immunol. 167:5122-5128(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
```



RN	[2]	SEQUENCE FROM N.A.
RP		TISSUE=Fetal liver;
RC		MEDLINE=20354998; PubMed=10894944;
RX		Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;
RA		"Molecular cloning and characterization of a mouse homolog of human
RT		TNFSF14, a member of the TNF superfamily.";
RL		Cytogenet. Cell Genet. 89:89-91(2000).
RN		[3]
RN		SEQUENCE FROM N.A.
RP		TISSUE=Lymphoma;
RC		Force W.R., Todd P.K., Mikayama T.;
RA		"Mouse LIGHT; molecular genetics, ligand binding and expression.";
RT		Submitted (JAN-2000) to the EMBL/GenBank/DBD databases.
RL		-I- FUNCTION: Cytokine that binds to TNFRSF3/LTRP. Binding to the
CC		decoy receptor TNFRSF6B modulates its effects. Activates NFkB and
CC		stimulates the proliferation of T cells.
CC		-I- SUBUNIT: Homotrimer (by similarity).
CC		-I- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC		similarity).
CC		-I- PTM: The soluble form derives from the membrane form by
CC		proteolytic processing.
CC		-I- SIMILARITY: Belongs to the tumor necrosis factor family.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration
CC		between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as its content is in no way
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC		or send an email to license@isb-sib.ch).
CC		-----
DR		EMBL; AF123385; AAF76453.1; -
DR		ENBL; AB029155; BAA89559.1; -
DR		ENBL; AP227533; AAF36722.1; -
DR		HSP; P01375; 4TSV.
DR		MGD; MG1.1355317; Tnfefl4.
DR		GO; GO:0043027; F:caspase inhibitor activity; ISS.
DR		GO; GO:0005102; F:receptor binding; ISS.
DR		GO; GO:0001719; P:inhibition of caspase activation; ISS.
DR		GO; GO:0005888; P:release of cytoplasmic sequestered NF-kappaB; ISS.
DR		GO; GO:0007165; P:signal transduction; ISS.
DR		GO; GO:0043029; P:T-cell homeostasis; ISS.
DR		GO; GO:0042098; P:T-cell proliferation; ISS.
DR		InterPro; IPR006053; TNF abc.
DR		InterPro; IPR006052; TNF family.
DR		InterPro; IPR008983; TNF like.
DR		InterPro; IPR003636; TNF_subf.
DR		Pfam; PF00229; TNF; 1.
DR		PRINTS; PR01234; TNECROSISFCT.
DR		ProDom; PD002012; TNF_subf; 1.
DR		PROSITE; PS00251; TNF_1; FALSE_NEG.
DR		PROSITE; PS00449; TNF_2; 1.
KW		Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
FT		CHAIN 1 239
FT		Tumor necrosis factor ligand superfamily
FT		member 14, membrane form.
FT		Tumor necrosis factor ligand superfamily
FT		member 14, soluble form.
FT		Cytoplasmic (Potential).
FT		SIGNAL-ANCHOR FOR TYPE II MEMBRANE
FT		protein (Potential).
FT		Extracellular (Potential).
FT		Cleavage (Potential).
FT		Potential,
FT		N-linked (GlcNAc...) (Potential).
FT		N-linked (GlcNAc...) (Potential).
FT		CARBHYD 191 191
FT		SEQUENCE 239 AA; 26338 MW; 217874AC71ADBE3 CRC64;
QY		Query Match 11.8%; Score 152.5; DB 1; Length 239;
		Best Local Similarity 29.2%; Pred.No. 0.00019;
		Matches 47; Conservative 25; Mismatches 72; Indels 17; Gaps 6;
OY		85 AAHITGRSGNTLSPNSKNEALCRKINSWESSRSGHSFLSNLRNGELVIHEKGFY 144

Db	93	AAHUTGANASLIGGGP-----LWE-TRLGLAFLRGLTYHDGALVTMEPGY	133			
Qy	145	YIYSQTYFRFOEEIKENTKNDQMVOYIKYKTS-YPDPILLMKKSARNCSWCKDAEYGLY-	202			
Db	140	YVYSKVQLS-GVGCPOGLANGLPITHGLYKRTSRYPKLELLVSRSPCGRANSRVWMD	198			
Qy	203	SIYOGGIFELKENDRIFVSVTNEHLI-DMDHEASFFGAPLV	242			
Db	199	SSFGLGGVVHLEAGEVVRVPCNRLVRPDGTRSYFGAFMV	239			
RESULT 9						
ID	Q7T2Q3	PRELIMINARY;	PRT; 227 AA.			
AC	O7T2Q3;					
DT	01-OCT-2003	(TrEMBLrel. 25, Created)				
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)				
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)				
DE	Tumor necrosis factor-3 alpha.					
GN	Name=TNF-3alpha;					
OS	Cyprinus carpio (Common carp).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;					
OC	Cyprinidae; Cyprinus.					
OX	NCBI_TaxID=7962;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Head kidney;					
RC	PubMed=15145420; DOI=10.1016/j.fsi.2003.11.001;					
RA	Savan R., Sakai M.;					
RT	"Presence of multiple isoforms of TNF alpha in carp (Cyprinus carpio					
RT	L.): genomic and expression analysis.";					
RL	Fish Shellfish Immunol. 17:87-94(2004).					
DR	EMBL; AB112424; BAC77690.1; -.					
DR	GO; GO:0016020; C:membrane; IEA.					
DR	GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.					
DR	GO; GO:0006955; P:immune response; IEA.					
DR	InterPro; IPR006052; TNF family.					
DR	InterPro; IPR008983; TNF_like.					
DR	InterPro; IPR003636; TNF_subf.					
DR	Pfam; PF00229; TNF; 1.					
DR	ProDom; PD002012; TNF_subf; 1.					
DR	SMART; SM00207; TNF; 1.					
DR	PROSITE; PS00049; TNF 2; 1.					
SQ	SEQUENCE 227 AA; 25226 MW; 010BC2B1E8D7265E CRC64;					
Query Match						
Best Local Similarity 25.3%; Score 151.5; DB 2; Length 227;						
Matches 45; Conservative 34; Mismatches 68; Indels 31; Gaps 7						
Qy	75	LVREERGQVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNG	134			
Db	67	LSKNVTSKVAIHLSGA-----YEPDVSKNIDMKQDGAFFVSGGLKLYDR	113			
Qy	135	ELVTHEKGFYIYSQTYFRFOEEIKENTKNDQMVOYIKYKTSYDP-----PILLMKSA	188			
Db	114	EIIIPNDGIFVIYSQVSEFHI--SCNDWTEQEVHSHAVFHKSDFFGIYKP--LIRAA	169			
Qy	189	RNSCW----SKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF	240			
Db	170	RSACVHASNTEDVWYD--TIYLGAAFSLRAGDKLCTKTTELLPRVETDNAKTPFGVF	225			
RESULT 10						
ID	O70332	PRELIMINARY;	PRT; 216 AA.			
AC	O70332;					
DT	01-AUG-1998	(TrEMBLrel. 07, Created)				
DT	01-AUG-1998	(TrEMBLrel. 07, Last sequence update)				
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)				
DE	Tumor necrosis factor-alpha (fragment).					
OS	Mesocricetus auratus (Golden hamster).					

DR GO: 0006955; P: immune response; IEA.  
DR InterPro: IPR006053; TNF\_abcd.  
DR InterPro: IPR002960; TNF\_beta.  
DR InterPro: IPR006052; TNF\_family.  
DR InterPro: IPR008983; TNF\_like.  
DR InterPro: IPR003636; TNF\_subf.  
DR Pfam: PF00229; TNF\_1.  
DR PRINTS: PR01234; TNECROSISFCT.  
DR PRINTS: PR01236; TNFBETA.  
DR PRODOM: PD002012; TNF\_subf; 1.  
DR SMART: SM00207; TNF; 1.  
DR PROSITE: PS50049; TNF\_2; 1.  
SQ SEQUENCE 241 AA; 26702 MW; 2C493CF80651EA2C CRC64;

Query Match 11.1%; Score 143; DB 2; Length 241;  
Best Local Similarity 24.3%; Pred. No. 0.0011;  
Matches 44; Conservative 34; Mismatches 87; Indels 16; Gaps 6;

Qy 75 LVRRGQRVAAHITGRSNTLS---PNSKNEKALGRKINSWESSRSGHSL-SNLH 130  
Db 60 LIRKDTAEKTPHVTLLKRISAKAAIHLEGSYEGEIVKDOLEWKNQ-GQAFAGQGF 118  
Qy 131 LRNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQMVQYIYKTSYDPDI----LIMK 186  
Db 119 LVNNQIVIPQGLYFVYCOASFRVSCNGDEGAGKGLTPLSHRIWYSDSIGSKASLVS 178  
Qy 187 SARNSCSKQDAE-----YGLY-SIYQGIPELKENDRIFVSVTNEHLIDMDHEASFFGA 239  
Db 179 AVRSACQSTTQEDSYRAGQGWYNTIYLGAVALNKGRLWTQPSLETDEGKTFFGV 238  
Qy 240 F 240  
Db 239 F 239

RESULT 12  
Q8AW02 PRELIMINARY; PRT; 231 AA.

ID Q8AW02  
AC Q8AW02;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative Tumour necrosis factor alpha two.  
GN Name=TNF-alpha2pro;  
OS Cyprinus carpio (Common carp).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Cyprinus.  
OX NCBI\_TaxID=7962;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Head kidney;  
RX MEDLINE=22365628; PubMed=12477499; DOI=10.1016/S0145-305X(02)00064-2;  
RA Saeij J.P., Stet R.J., de Vries B., van Muiswinkel W.B.,  
RA Wiegertjes G.F.;  
RT "Molecular and functional characterization of carp TNF: a link between  
RT TNF polymorphism with trypanotolerance?";  
RL Dev. Comp. Immunol. 27:29-41(2003).  
DR EMBL: AJ311801; CAC84642.2; -.  
DR HSSP: P01375; 4TSV.  
DR GO: 0016020; C:membrane; IEA.  
DR GO: 0005164; F:tumor necrosis factor receptor binding; IEA.  
DR GO: 0006955; P:immune response; IEA.  
DR InterPro: IPR006053; TNF\_abcd.  
DR InterPro: IPR002960; TNF\_beta.  
DR InterPro: IPR006052; TNF\_family.  
DR InterPro: IPR008983; TNF\_like.  
DR Pfam: PF00229; TNF; 1.  
DR PRINTS: PR01234; TNECROSISFCT.  
DR PRODOM: PD002012; TNF\_subf; 1.  
DR SMART: SM00207; TNF; 1.  
DR PROSITE: PS50049; TNF\_2; 1.  
DR PROSITE: PS50049; TNF\_2; 1.  
KW Signal.  
FT SIGNAL. 1 20 Potential.  
FT CHAIN 80 >232 tumor necrosis factor.  
FT NON TER 232 232  
SQ SEQUENCE 232 AA; 25704 MW; E48A9379DB4F216D CRC64;

DR PROSITE: PS50049; TNF\_2; 1.  
SQ SEQUENCE 231 AA; 25927 MW; 2AD8871D0B1A82F1 CRC64;

Query Match 11.0%; Score 141; DB 2; Length 231;  
Best Local Similarity 23.3%; Pred. No. 0.0016;  
Matches 51; Conservative 38; Mismatches 90; Indels 40; Gaps 9;

Qy 44 WQLRQLVRKMLRTSEETISTVQEKQON-----ISPLVRGQRPQVAHITGR 92  
Db 29 WRVCGVLLAVALCAAAAVCFTLKSNQNEGNALRLTLRDHLKSNVTSKVAIHLTGA- 87  
Qy 93 GRSNTLSSPNSKNEKALGRKINSWESSRSGHSLSNLHRLNGELVIHEKGFYIYSQTYF 152  
Db 88 -----YDPDVCKNDL-----DWKQNDQAFVSGGLELVDRILIPNDGIYFVYSQSF 135  
Qy 153 RFQBEIKENTKNDKQMV-----QYIYKTSYDPDILLMKASRNSC-WSKDASYGLY-S 203  
Db 136 HI--SKDHMTEDQDVVHMSHAVLRYSESYGSKP---LFSAIRSACVHSDSEDLWTNT 190  
Qy 204 IYQGIPELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240  
Db 191 IYLGAAFLNLRARDRLRTETTKELLPRVSENGKTFPGVF 229

RESULT 13  
Q80XA4 PRELIMINARY; PRT; 232 AA.

ID Q80XA4  
AC Q80XA4;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Tumor necrosis factor precursor (fragment).  
GN Name=Tnf;  
OS Peromyscus maniculatus (Deer mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
OC Peromyscus.  
OX NCBI\_TaxID=10042;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Green R.M., Herbat M.M., Schountz T.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY249143; AAP03078.1; -.  
DR HSSP: P06804; 2TNF.  
DR GO: 0016020; C:membrane; IEA.  
DR GO: 0005164; F:tumor necrosis factor receptor binding; IEA.  
DR GO: 0006955; P:immune response; IEA.  
DR InterPro: IPR006053; TNF\_abcd.  
DR InterPro: IPR002959; TNF\_alpha.  
DR InterPro: IPR006052; TNF\_family.  
DR InterPro: IPR008983; TNF\_like.  
DR InterPro: IPR003636; TNF\_subf.  
DR Pfam: PF00229; TNF; 1.  
DR PRINTS: PR01234; TNECROSISFCT.  
DR PRINTS: PR01235; TNFALPHA.  
DR PRODOM: PD002012; TNF\_subf; 1.  
DR SMART: SM00207; TNF; 1.  
DR PROSITE: PS00251; TNF\_1; 1.  
DR PROSITE: PS50049; TNF\_2; 1.  
DR PROSITE: PS50049; TNF\_2; 1.  
KW Signal.  
FT SIGNAL. 1 20 Potential.  
FT CHAIN 80 >232 tumor necrosis factor.  
FT NON TER 232 232  
SQ SEQUENCE 232 AA; 25704 MW; E48A9379DB4F216D CRC64;

Query Match 10.7%; Score 137.5; DB 2; Length 232;  
Best Local Similarity 24.5%; Pred. No. 0.003;  
Matches 45; Conservative 36; Mismatches 78; Indels 25; Gaps 8;

Qy 72 ISPLVRGQRPQVAHITGRSNTL--SSPNSKNEKALGRKINS-----WESSRSG 122  
Db 56 IGFOREKEFPNNLP--IIGSWAQTLTLRSSQNSDKPVAHVAVHNVQVDEQLWLSRAN 113

```
Qy 123 HSFUSNHLNGLVILVHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKY-TSYDPDP 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 ALLANGMDLKDQNLVDPADGLYLYVSQVLFKQG-----GCSNYLLTHTVSRFAVSYEDK 168
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 182 ILLMKARSNCWSKDAEYV-----LVSIVGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 169 VNLUSATKSPC-PKETPEGSELKPWBPYILGVGFQLEKGRDLSAEVNLPRYLDFABSQG 227
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 236 -FFG 238
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 VYFG 231

RESULT 14
Q6T9C7 PRELIMINARY; PRT; 234 AA.
AC Q6T9C7,
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Tumor necrosis factor.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Phelan P.E. III, Mellon M.M., Kim C.H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY427649; AAR06286.1; -.
DR HSP; P01375; IABM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_abcd.
DR InterPro; IPR002960; TNF_beta.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRINTS; PR01236; TNFBETA.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 234 AA; 25826 MW; 6588DCF46D3F131C CRC64;

Query Match 10.7%; Score 137.5; DB 2; Length 234;
Best Local Similarity 26.4%; Pred. No. 0.0031;
Matches 51; Conservative 30; Mismatches 83; Indels 29; Gaps 8;

Qy 61 TISTVQEKQNIPL-----VNERGQ-----RVAHIHTGRSNTLSSPNKSKALGRK 112
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 56 TLHKTQNGQDGSVLRITLDRISQGNFTSKAAIHLTG-----GYNSES-----K 100
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 113 INSWESSRSGHSFLSNLHNLNGLVILVHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYI 172
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 101 TLDRDDQDQAFSSGGLKLVNREIIIPDDGIFYFYSQVSLHI-SCSELTEEQVLMASHV 159
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 173 YKVT-SYDPFILMKARSNCWSKDAEYGLY--SIYGGIFELKENDRIFVSVTNEHL-- 227
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 MRFSESYGGKKPLPSAIRSICTQPESENLYWNTIYLGAAPHLREGDRLGDTTALLPM 219
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 228 IDMDHEASFFGAF 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 220 VENDNGKTFPGVF 232

RESULT 15
TNFA_RABIT
ID -TNFA_RABIT
AC P04924;
```



DR Pfam: PF00229; TNF; 1.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR PRODOM; PD002012; TNF\_subf; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS0049; TNF\_2; 1.  
KW Cytokine; Phosphorylation; Signal-anchor; Transmembrane.  
FT CHAIN 1 235  
FT CHAIN 80 235 Tumor necrosis factor, membrane form.  
FT DOMAIN 1 35 Cytoplasmic (Potential).  
FT TRANSMEM 36 56 Signal-anchor for type II membrane protein (Potential).  
FT DOMAIN 57 235 Extracellular (Potential).  
FT SITE 79 80 Cleavage (by ADAM17) (By similarity).  
FT MOD\_RES 2 2 Phosphoserine (by CK1) (By similarity).  
FT DISULFID 148 179 By similarity.  
FT CONFLICT 63 63 Missing (in Ref. 3).  
SQ SEQUENCE 235 AA; 25816 MW; 610177D0BD2BF871 CRC64;

Query Match 10.6%; Score 136.5; DB 1; Length 235;  
Best Local Similarity 23.0%; Pred. No. 0.0037;  
Matches 42; Conservative 37; Mismatches 81; Indels 23; Gaps 7;

Qy 72 ISPLVREGRQORVAAHITGTRGNLT-SSPNSKNEKALGRKINS-----WESSRSG 122  
Db 56 IGPOEEEQSPNNL--HLVNPVQAQWTLRSARALSDKPLAHVNPQVEGOLQWLSORAN 113  
Qy 123 HSFPLSNLHRLNGELVIEHKGFFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKY-TSYDPDP 181  
Db 114 ALLANGMKLTQNLQVLPADGLYLIYSQVLFSGQ-----GCRSYVLLTHTVSRFAVSYPNK 168  
Qy 182 ILLMKSARNSCWSKDAEY-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS- 235  
Db 169 VNLLSAIKSPCHRETPBEAEPMAWYEPIYLGGVFQLEKGRDLSTEVNQPEYLDLAESQV 228  
Qy 236 FFG 238  
Db 229 YFG 231

Search completed: June 3, 2005, 06:43:56  
Job time : 176 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model  
Run on: June 3, 2005, 06:25:45 ; Search time 151 Seconds  
(without alignments)  
583.744 Million cell updates/sec

Title: US-10-662-431-2\_COPY\_39\_281  
Perfect score: 1287  
Sequence: 1 TNELKQMDKYSKSIACFL.....NEHLIDMDHEASFFGAFVIG 243

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1523986

Minimum DB seq length: 0  
Maximum DB seq length: 243

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: geneseqp1980a:.\*  
2: geneseqp1990a:.\*  
3: geneseqp2000a:.\*  
4: geneseqp2001a:.\*  
5: geneseqp2002a:.\*  
6: geneseqp2003a:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004a:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	958	74.4	187	8	ADN35127 Human TRA
2	953.5	74.1	220	3	AAY88630 Cell fact
3	907	70.5	173	5	ABG72258 Partial h
4	887	68.9	168	4	ABG76826 Human TRA
5	887	68.9	168	5	AU99896 Human TNF
6	882	68.5	168	5	ABG72259 Partial h
7	878	68.2	166	3	ABR08274 Amino aci
8	866	67.3	167	6	ABR84402 TRAIL ani
9	850	66.0	161	4	AAY71985 C-termina
10	850	66.0	161	6	ABR39855 TNF fami
11	850	66.0	161	7	ADC03335 Tumour ne
12	827	64.3	212	5	AU99301 Human TRA
13	764.5	59.4	154	7	AD153053 Human TRA
14	764	59.4	171	8	ADO24774 Cat solub
15	764	59.4	201	8	ADO24776 Cat solub
16	746.5	58.0	188	5	AU79599 Human TRA
17	727	56.5	139	2	AAY01518 Polypepti
18	711.5	55.3	172	8	ADO24770 Dog solub
19	711.5	55.3	207	8	ADO24772 Dog solub
20	633	49.2	172	3	ABO8275 Amino aci
21	544	42.3	169	8	AD198264 Human TNF
22	425	33.0	121	3	AG03752 Human sec
23	370	28.7	113	5	AU79600 Human TRA
24	292	22.7	120	8	AD198267 Human TRA
25	291	22.6	98	5	Aau79595 Human TNF

26	291	22.6	98	8	ABO84414	Human can
27	291	22.6	101	2	AAW19790	Human apo
28	291	22.6	101	2	AAW56761	Human TRA
29	291	22.6	101	4	AAE11032	Human TRA
30	291	22.6	101	6	ABU08559	Human TNF
31	291	22.6	101	8	ADK15500	Human TRA
32	291	22.6	122	8	ADL98266	Human TNF
33	278	21.6	56	5	AAE23263	Protein #
34	277	21.5	88	5	AAU79594	Human TRA
35	236	18.3	178	6	ADA50080	Human wll
36	233.5	18.1	199	5	ABG94285	Mouse ran
37	233.5	18.1	199	5	ABG80597	Mouse rec
38	233.5	18.1	199	7	ADJ82119	Protein f
39	232.5	18.1	152	4	ABG67248	Human RAN
40	232.5	18.1	158	7	ADJ82134	Protein f
41	232.5	18.1	159	7	ADJ82117	Protein f
42	232.5	18.1	160	3	AAO8273	Amino aci
43	232.5	18.1	165	7	ADJ82136	Protein f
44	232.5	18.1	178	7	ADJ82116	Protein f
45	232.5	18.1	180	7	ADJ82133	Protein f

ALIGNMENTS

RESULT 1  
ADN35127  
ID ADN35127 standard; protein; 187 AA.  
XX  
AC ADN35127;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human TRAI-1 extracellular region.  
XX  
KW human TRAI-1 extracellular region; antineoplastic.  
XX  
OS Homo sapiens.  
XX  
PN CN1436792-A.  
XX  
PD 20-AUG-2003.  
XX  
PF 08-FEB-2002; 2002CN-00104519.  
XX  
PR 08-FEB-2002; 2002CN-00104519.  
XX  
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.  
XX  
PI Zheng D, Liu Y, Shi J;  
XX  
DR WPI; 2004-023846/03.  
XX  
PT New tumor necrosis factor relative cell death inducing ligand  
extracellular region mutation polypeptide, used for an antineoplastic  
application.  
XX  
PS Claim 1; SEQ ID NO 1; 15pp; Chinese.  
XX  
CC The present invention provides one kind of mutant 95-281 recombinant  
soluble polypeptide (rsTRAILrh95gly-281) in human TRAIL extracellular  
region. The preparation process and antineoplastic application of the  
recombinant soluble polypeptide are also provided. The present sequence  
represents human TRAI-1 extracellular region.  
XX  
SQ Sequence 187 AA;

Query Match 74.4%; Score 958; DB 8; Length 187;  
Best Local Similarity 98.9%; Pred. NO. 3e-85;  
Matches 184; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 SEETISTVOEKQONISPLVRGPGVAAHITGTRNTLTSSPNKKEKALGRINSWE 117  
|||||

Db 2 SEETISTVQEKQONISPLVRRGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 61

Qy 118 SSRSGHSFLSNLHRLNGELVHKEGFFYYISQTYFRFOEEIKENTKNDKQMVQIYKYTS 177

Db 62 SSRSGHSFLSNLHRLNGELVHKEGFFYYISQTYFRFOEEIKENTKNDKQMVQIYKYTS 121

Qy 178 YPDPILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 237

Db 122 YPDPILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 181

Qy 238 GAFLVG 243

Db 182 GAFLVG 187

RESULT 2

ID AAY88630 standard; protein; 220 AA.

XX AC AAY88630;

XX AC

XX 22-AUG-2000 (first entry)

XX DE Cell factor derivative TRAILD amino acid sequence.

XX KW Cell factor derivative; TRAILD; anticancer; cancer; liver; breast;

XX KW kidney; leukaemia.

XX OS Unidentified.

XX FN CN1243748-A.

XX PD 09-FEB-2000.

XX XX 28-JUL-1999; 99CN-00111039.

XX PR 28-JUL-1999; 99CN-00111039.

XX PA (BASI-) INST BASIC MEDICAL SCI CHINESE ACAD MEDI.

XX PI Zheng D, Liu Y, Ma Z;

XX XX WPI; 2000-351201/31.

XX PT New cell factor derivative causing cells to die, for anticancer therapy.

XX PS Disclosure; Page 2; 10pp; Chinese.

XX CC The present invention relates to a cell factor derivative (TRAILD) used

CC as an anticancer derivative. The TRAIL protein can be expressed in

CC soluble form in bacterial cytoplasm. The present sequence represents a

CC TRAILD amino acid sequence. Recombinant TRAILD fusion proteins can be

CC used in anti-cancer medicaments to treat cancer of the liver, breast, or

CC kidney. It can also be used to treat leukaemia

XX SQ Sequence 220 AA;

Query Match 74.1%; Score 953.5; DB 3; Length 220;

Best Local Similarity 97.9%; Pred. No. 1.1e-84;

Matches 185; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 56 RTSEETISTVQEKQONISPLVRRGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINS 115

Db 32 KTSEETISTVQEKQONISPLVRRGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINS 91

Qy 116 WESSRSGHSFLSNLHRLNGELVH- EKGFFYYISQTYFRFOEEIKENTKNDKQMVQIYK 174

Db 92 WESSRSGHSFLSNLHRLNGELVHKEGFFYYISQTYFRFOEEIKENTKNDKQMVQIYK 151

Qy 175 YTSYDPDILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 234

Db 152 YTSYDPDILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 211

Qy 235 SFFGAFLVG 243

Db 212 SFFGAFLVG 220

RESULT 3

ID ABG72258 standard; protein; 173 AA.

XX AC ABG72258;

XX 04-MAR-2003 (first entry)

XX DE Partial human Trail protein, Trail109.

XX KW Human; tumour related apoptosis inducing ligand; Trail109;

XX KW Trail prokaryotic expression system; tumour cell death.

XX OS Homo sapiens.

XX FT Key Location/Qualifiers

FT Misc-difference 109

FT /note= "Encoded by CTT"

XX FN CN1354183-A.

XX PD 19-JUN-2002.

XX PF 30-NOV-2001; 2001CN-00132371.

XX PR 30-NOV-2001; 2001CN-00132371.

XX PA (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.

XX PI Hu Y, Yao Y;

XX DR WPI; 2002-751439/82.

XX DR N-PSDB; ABX14392.

XX PT Tumor death induction ligand gene, gene expression protein and its

XX PT preparation method.

XX PS Claim 7; Page 10 (disclosure); 17pp; Chinese.

XX CC The present invention relates to the isolation of cDNA encoding human

CC tumour related apoptosis inducing ligand (Trail), and the Trail protein.

CC The Trail full length cDNA is cloned, and is utilised to create a Trail

CC prokaryotic expression system. The full length Trail cDNA is used to

CC respectively clone cDNA of soluble ectocytic segment Trail109 and Trail

CC 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic

CC expression systems. The prokaryotic expression systems created greatly

CC increase the expression and quantity of the Trail, Trail109, and Trail114

CC proteins, and may be useful in a new preparation for killing tumour

CC cells. The present sequence represents the partial human Trail protein,

XX CC Trail109

XX SQ Sequence 173 AA;

Query Match 70.5%; Score 907; DB 5; Length 173;

Best Local Similarity 99.4%; Pred. No. 2.7e-80;

Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 71 NISPLVRERQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLH 130

Db 1 NISPLVRERQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLH 60

Qy 131 LRNGELVHKEGFFYYISQTYFRFOEEIKENTKNDKQMVQIYKYTSYPPDILLMKSARN 190

Db 61 LRNGELVHKEGFFYYISQTYFRFOEEIKENAKNDKQMVQIYKYTSYPPDILLMKSARN 120

Qy 191 SCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243

Db 121 SCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 173

```
RESULT 4
ABB76826 ID ABB76826 standard; protein; 168 AA.
XX AC ABB76826;
XX DT 16-JUL-2002 (first entry)
XX DE Human TRAIL.
XX KW Human; TRAIL; tumour necrosis factor; TNF;
XX KW tumour necrosis factor related apoptosis inducing ligand; TRAIL; cancer;
XX KW viral infection; cytostatic.
XX OS Homo sapiens.
XX PN KR2001019100-A.
XX PD 15-MAR-2001.
XX PF 25-AUG-1999; 99KR-00035354.
XX PR 25-AUG-1999; 99KR-00035354.
XX PA (DONG-) DONG WHA PHARM IND CO LTD.
XX PI Cha SS, Kim JU, Lee GJ, Lim GM, Oh BH, Yoon JI, Yoon SJ;
XX WPI; 2001-533833/59.
XX DR N-PSDB; ABL53366.
XX PT Producing and crystallizing tumor necrosis factor related apoptosis
XX PT inducing ligand protein, and its three-dimensional structure.
XX PS Claim 1; Page 14; 20pp; Korean.
XX CC The present invention relates to a method for producing Tumour Necrosis
XX CC Factor (TNF) Related Apoptosis Inducing Ligand (TRAIL) protein, and for
XX CC crystallising the TRAIL protein and its three-dimensional structure,
XX CC where the TRAIL protein has improved activity, which specifically kills
XX CC cancer cells and cells infected by virus. The present sequence is human
XX CC TRAIL, which was used in the invention
XX SQ Sequence 168 AA;
Query Match 68.9%; Score 887; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 76 VRERGQPVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 135
DB 1 VRERGQPVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 60
QY 136 LVIHEKGFYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYDPDILLMKSARNCSWK 195
DB 61 LVIHEKGFYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYDPDILLMKSARNCSWK 120
QY 196 DAEGYLSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 243
DB 121 DAEGYLSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 168
RESULT 5
AAU99896 ID AAU99896 standard; protein; 168 AA.
XX AC AAU99896;
XX DT 21-OCT-2002 (first entry)
XX DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
```

```
XX TRAIL; TNF receptor apoptosis including ligand; human; SDR5;
KW tumour necrosis factor; crystal structure; TRAIL-SDR5 complex; apoptosis.
XX OS Homo sapiens.
XX PN WO200253727-A1.
XX PD 11-JUL-2002.
XX PF 10-JAN-2001; 2001WO-KR000034.
XX PR 29-DEC-2000; 2000KR-00085947.
XX PA (DONG-) DONG WHA PHARM IND CO LTD.
XX PA (UYPO-) UNIV POHANG SCI & TECHNOLOGY.
XX PI Chung YH, Ryu JM, Hwang YH, Yoon JI, Lim KM, Oh B, Cha S;
XX WPI; 2002-583613/62.
XX Novel expression vector containing an sDR5 encoding gene transformed into
XX PT Escherichia coli to produce sDR5 protein for crystallizing a tumor
XX PT necrosis factor-related apoptosis-inducing ligand-sDR5 complex.
XX PS Claim 5; Page 70; 74pp; English.
XX CC This invention relates to an expression vector containing the tumour
XX CC necrosis factor related apoptosis inducing ligand (TRAIL) protein
XX CC receptor SDR5. The invention also comprises a method for producing the
XX CC SDR5 protein from an E. coli transformed with the vector. The method of
XX CC the invention is useful for crystallising the TRAIL-SDR5 complex. A TRAIL
XX CC -SDR5 crystal complex is useful for developing recombinant proteins i.e.
XX CC proteins with improved stability or cytotoxic activity of a TRAIL protein
XX CC which involves changing the amino acid of the AA loop to increase the
XX CC various interactions between amino acids or from the binding site of
XX CC metal ions or the disulfide bonding, or changing the corresponding amino
XX CC acids of the homotrimer interface or homodimer interface to increase the
XX CC various interactions between amino acids or from the binding site of
XX CC metal ion or disulfide bond, or to fill the cavity. A 3 dimensional
XX CC structure of the TRAIL-SDR5 complex is useful for the molecular strategy
XX CC conferring specificity for the recognition between TNF family members and
XX CC TNF receptor family members and for the development of TRAIL protein,
XX CC which has a better stable, cytotoxic activity or an improved receptor
XX CC binding affinity. The present sequence represents the human tumour
XX CC necrosis factor receptor apoptosis including ligand (TRAIL) protein
XX CC sequence used in the invention
XX SQ Sequence 168 AA;
Query Match 68.9%; Score 887; DB 5; Length 168;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 76 VRERGQPVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 135
DB 1 VRERGQPVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 60
QY 136 LVIHEKGFYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYDPDILLMKSARNCSWK 195
DB 61 LVIHEKGFYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYDPDILLMKSARNCSWK 120
QY 196 DAEGYLSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 243
DB 121 DAEGYLSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 168
RESULT 6
ABG72259 ID ABG72259 standard; protein; 168 AA.
XX AC ABG72259;
XX DT 21-OCT-2002 (first entry)
XX DE Human TNF related apoptosis including ligand (TRAIL) protein.
```

DT 04-MAR-2003 (first entry)  
 XX Partial human Trail protein, Traill114.  
 DE Human; tumour related apoptosis inducing ligand; Traill114;  
 XX Trail prokaryotic expression system; tumour cell death.  
 KW Homo sapiens.  
 XX  
 OS  
 PH Key Location/Qualifiers  
 FT Misc-difference 104  
 FT /note= "Encoded by CTT"  
 XX  
 XX CN1354183-A.  
 XX 19-JUN-2002.  
 PD  
 XX 30-NOV-2001; 2001CN-00132371.  
 PF  
 XX 30-NOV-2001; 2001CN-00132371.  
 PR  
 XX (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.  
 PA  
 XX Hu Y, Yao Y;  
 PI  
 XX WPI; 2002-751439/82.  
 DR  
 XX N-PSDB; ABX14393.  
 DR  
 XX  
 XX Tumor death induction ligand gene, gene expression protein and its  
 PT preparation method.  
 PT  
 XX  
 XX Claim 7; Page 10 (disclosure); 17pp; Chinese.  
 PS  
 XX The present invention relates to the isolation of cDNA encoding human  
 CC tumour related apoptosis inducing ligand (Trail); and the Trail protein.  
 CC The Trail full length cDNA is cloned, and is utilised to create a Trail  
 CC prokaryotic expression system. The full length Trail cDNA is used to  
 CC respectively clone cDNA of soluble ectocytic segment Trail109 and Trail  
 CC 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic  
 CC expression systems. The prokaryotic expression systems created greatly  
 CC increase the expression and quantity of the Trail, Trail109, and Trail114  
 CC proteins, and may be useful in a new preparation for killing tumour  
 CC cells. The present sequence represents the partial human Trail protein,  
 CC Trail114  
 CC  
 XX  
 SQ Sequence 168 AA;  
 Query Match 68.5%; Score 882; DB 5; Length 168;  
 Best Local Similarity 99.4%; Pred. No. 7.2e-78;  
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 76 VREGPQVAAHITGTRGSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHLRNGE 135  
 Db 1 VREGPQVAAHITGTRGSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHLRNGE 60  
 Qy 136 LVIHEKGFYIYSQTYFRFOBEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSK 195  
 Db 61 LVIHEKGFYIYSQTYFRFOBEIKENAKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSK 120  
 Qy 196 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243  
 Db 121 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 168  
 RESULT 7  
 AAB08274  
 ID AAB08274 standard; protein; 166 AA.  
 XX  
 AC AAB08274;  
 XX  
 DT 04-DEC-2000 (first entry)  
 XX  
 XX Amino acid sequence of a human TNF ligand TRAIL.

XX AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;  
 KW type II transmembrane protein; B cell stimulatory factor;  
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;  
 KW lupus and graft versus host disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200047740-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 XX 11-FEB-2000; 2000WO-US003653.  
 XX  
 XX 12-FEB-1999; 99US-0119906P.  
 PR  
 XX 18-NOV-1999; 99US-0166271P.  
 PR  
 XX (AMGE-) AMGEN INC.  
 PA  
 XX Boyle WJ, Hsu H;  
 XX  
 XX WPI; 2000-558217/51.  
 DR  
 XX Novel polypeptides comprising tumor necrosis factor ligand family  
 PT proteins, useful for treating inflammatory and immune disorders, e.g.  
 PT rheumatoid arthritis.  
 PT  
 XX Claim 14; Fig 9; 71pp; English.  
 PS  
 XX AAB08265-83 represent tumour necrosis factor (TNF) ligands. The  
 CC specification describes an AGP-3 polypeptide, which is TNF ligand family  
 CC member. AGP-3 is a type II transmembrane protein, and is a potent B cell  
 CC stimulatory factor. Expression of AGP-3 correlates to increases in the  
 CC number of B cells and immunoglobulins produced. AGP-3 proteins,  
 CC antibodies, and nucleic acids may be used to treat inflammatory and  
 CC immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and  
 CC graft versus host disease. The nucleic acids may be used to regulate the  
 CC expression of an AGP-3 related protein. The AGP-3 proteins, antibodies  
 CC and nucleic acids are also useful for the detection of AGP-3 agonists,  
 CC antagonists and characterizing interactions with AGP-3 related proteins  
 CC  
 XX  
 SQ Sequence 166 AA;  
 Query Match 68.2%; Score 878; DB 3; Length 166;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-77;  
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 78 ERGPQVAAHITGTRGSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 137  
 Db 1 ERGPQVAAHITGTRGSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV 60  
 Qy 138 IHEKGFYIYSQTYFRFOBEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSKDA 197  
 Db 61 IHEKGFYIYSQTYFRFOBEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSKDA 120  
 Qy 198 EYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243  
 Db 121 EYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 166  
 RESULT 8  
 ABR84402  
 ID ABR84402 standard; protein; 167 AA.  
 XX  
 AC ABR84402;  
 XX  
 DT 09-OCT-2003 (first entry)  
 XX  
 XX TRAIL amino acid sequence.  
 XX  
 XX TRAIL; TNF-related apoptosis-inducing ligand; tumour; necrosis.  
 XX  
 OS Unidentified.

XX CNI380339-A.  
XX 20-NOV-2002.  
XX 10-APR-2001; 2001CN-00105946.  
XX 10-APR-2001; 2001CN-00105946.  
XX (CHEN-) CHENGDU DIAO PHARM GROUP CO LTD.  
XX Li B, Gao X, Liu Z;  
XX WPI; 2003-230973/23.  
XX N-PSDB; ACC83357.  
XX Death induced ligand (TRAIL) cDNA and encoded polypeptide, useful for  
XX inducing the death of tumor cells, is related to mutational human tumor  
XX necrosis.  
XX Claim 4; Fig 2; 14pp; Chinese.  
XX The invention relates to a TNF-related apoptosis-inducing ligand encoding  
XX (TRAIL) cDNA and its encoded polypeptide. The gene of the invention is  
XX related to mutational human tumor necrosis. The polypeptide of the  
XX invention is useful for inducing the death of tumour cells. The current  
XX sequence represents the TRAIL amino acid sequence  
XX  
XX Sequence 167 AA;  
XX  
XX Query Match 67.3%; Score 866; DB 6; Length 167;  
XX Best Local Similarity 98.2%; Pred. No. 2.6e-76;  
XX Matches 166; Conservative 1; Mismatches 0; Indels 2; Gaps 1;  
QY 75 LVREGRQVAAHTGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNG 134  
Db 1 MVRERG--RVAAHTGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNG 58  
QY 135 ELVIERKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWS 194  
Db 59 ELVIERKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWS 118  
QY 195 KDAEYGLYSIQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 243  
Db 119 KDAEYGLYSIQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 167  
RESULT 9  
AAY71985  
ID AAY71985 standard; protein; 161 AA.  
XX AC AAY71985;  
XX 28-MAR-2001 (first entry)  
XX C-terminal region of human TRAIL protein.  
XX Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;  
XX Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1;  
XX therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;  
XX systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;  
XX thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;  
XX haemolytic anaemia; Grave's disease; myasthenia gravis; TRAIL protein;  
XX post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;  
XX B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Region 2..8  
XX /label= Beta\_strand  
XX Region 32..34  
XX /label= Beta\_strand

FT Region 42..44  
FT /label= Beta\_strand  
FT Region 47..50  
FT /label= Beta\_strand  
FT Region 53..56  
FT /label= Beta\_strand  
FT Region 61..72  
FT /label= Beta\_strand  
FT Region 86..91  
FT /label= Beta\_strand  
FT Region 99..109  
FT /label= Beta\_strand  
FT Region 118..128  
FT /label= Beta\_strand  
FT Region 133..143  
FT /label= Beta\_strand  
FT Region 153..160  
FT /label= Beta\_strand  
XX  
XX WO200068378-A1.  
XX  
XX 16-NOV-2000.  
XX  
XX 05-MAY-2000; 2000WO-US012266.  
XX  
XX 06-MAY-1999; 99US-0132892P.  
XX  
XX 01-MAY-2000; 2000US-0201012P.  
XX  
XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.  
XX  
XX Shu HS;  
XX  
XX WPI; 2001-016094/02.  
XX  
XX Isolated TALL-1 protein is used to identify compounds that regulate B  
XX lymphocyte proliferation, used to treat B lymphocyte associated  
XX autoimmune disorders.  
XX  
XX Example 1; Fig 1b; 112pp; English.  
XX  
XX The present invention relates to Tumour necrosis factor (TNF) and ApoL-  
XX related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,  
XX proteins (including homologues), and their antibodies. The invention in  
XX particular relates to methods for regulating the interaction between TALL  
XX -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to  
XX regulate monocyte, macrophage and B lymphocyte mediated immune responses.  
XX TALL-1 protein is useful for identifying compounds that regulate B  
XX lymphocyte proliferation. It is also useful for treating B lymphocyte  
XX associated autoimmune disorders like rheumatoid arthritis, systemic lupus  
XX erythematosus (SLE), insulin dependent diabetes mellitus, multiple  
XX sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic  
XX anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,  
XX pemphigus vulgaris, acute rheumatic fever, post-streptococcal  
XX glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its  
XX corresponding nucleic acid sequence are also useful in diagnostic assays.  
XX The present sequence is a C-terminal region of human TRAIL protein, which  
XX has 20-25% sequence identity with the C-terminal region of human TALL-1  
XX protein extracellular domain. TRAIL protein is a TNF family member  
XX  
XX Sequence 161 AA;  
XX  
XX Query Match 66.0%; Score 850; DB 4; Length 161;  
XX Best Local Similarity 100.0%; Pred. No. 9.2e-75;  
XX Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 83 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 142  
Db 1 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 60  
QY 143 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWSKDAEYGLY 202  
Db 61 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWSKDAEYGLY 120

Qy 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243  
 |||||  
 Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161

RESULT 10  
 ABR39855  
 ID ABR39855 standard; protein; 161 AA.  
 XX  
 AC ABR39855;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE TNF family member, TRAIL (1d4v) protein fragment.  
 XX  
 KW RANK; receptor activator of necrosis factor kB; RANK ligand; RANKL;  
 KW tumour necrosis factor; TNF; TRAIL; cytokine.  
 XX  
 OS Unidentified.  
 XX  
 PN W02003014077-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 09-AUG-2002; 2002WO-US025287.  
 XX  
 PR 09-AUG-2001; 2001US-0311163P.  
 PR 22-MAR-2002; 2002US-00105057.  
 XX  
 PA (BARN-) BARNES-JEWISH HOSPITAL.  
 XX  
 PI Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;  
 XX WPI; 2003-256526/25.  
 XX  
 PT Composition for identifying a compound with Receptor Activator of  
 PT Necrosis Factor kB, RANK modulating activity and for identifying RANK or  
 PT osteoprotegerin modulating compound, has a protein complex in crystalline  
 PT form.  
 XX  
 PS Disclosure; Fig 3; 66pp; English.

XX The invention relates to a composition (I) comprising a protein complex  
 CC in crystalline form, where the complex comprises an amino acid sequence  
 CC of a Receptor Activator of Necrosis Factor kB (RANK) Ligand (RANKL)  
 CC ectodomain. (I) is useful for identifying a compound with RANK modulating  
 CC activity, and for identifying a RANK or OPG modulating compound. (I) is  
 CC useful to intelligently design mutants that have altered biological  
 CC properties and for identifying and/or designing compounds that bind RANK  
 CC as an approach towards developing new therapeutic agents. (I) is also  
 CC useful to computationally screen small molecule databases for chemical  
 CC entities or compounds that can bind in whole, or in part, to RANK or  
 CC RANKL. The present sequence represents a tumour necrosis factor (TNF)  
 CC family member, TRAIL (1d4v), used in a structural-based alignment study  
 CC of murine RANKL protein  
 XX  
 SQ Sequence 161 AA;

Query Match 66.0%; Score 850; DB 6; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-75;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 RVAAHITGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 142  
 |||||  
 Db 1 RVAAHITGRSNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 60  
 |||||  
 Qy 143 FYIYSQTYFRFQBEIKENTKNDQMVQYIKYTSYDPDILLMKSARNCSWSDAEYGLY 202  
 |||||  
 Db 61 FYIYSQTYFRFQBEIKENTKNDQMVQYIKYTSYDPDILLMKSARNCSWSDAEYGLY 120  
 |||||  
 Qy 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243  
 |||||  
 Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161

RESULT 11  
 ADC03335  
 ID ADC03335 standard; protein; 161 AA.  
 XX  
 AC ADC03335;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Tumour necrosis factor family cytokine, TRAIL.  
 XX  
 KW RANKL ectodomain crystal complex; RANK; osteoprotegerin; OPG;  
 KW bone-forming compound; tumour necrosis factor; TNF family; cytokine;  
 KW TRAIL.  
 XX  
 OS Mus sp.  
 XX  
 PN US2003050223-A1.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 09-AUG-2002; 2002US-00215446.  
 XX  
 PR 09-AUG-2001; 2001US-0311163P.  
 XX  
 PA (LAMJ/) LAM J.  
 PA (ROSS/) ROSS F P.  
 PA (TEIT/) TEITELBAUM S L.  
 PA (NELS/) NELSON C A.  
 PA (FREM/) FREMONT D H.  
 XX  
 PI Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;  
 XX WPI; 2003-605763/57.  
 XX  
 PT Composition comprising crystalline receptor activator of NfkappaB (RANK)  
 PT ligand ectodomain complex whose three-dimensional structural  
 PT representation is useful for identifying RANK or osteoprotegerin  
 PT modulating compound.

XX Disclosure; Fig 3; 40pp; English.

XX The invention relates to a composition comprising a protein complex in  
 CC crystalline form, where the complex comprises an amino acid sequence of a  
 CC receptor activator of nuclear factor kappaB (NfkappaB) (RANK) ligand  
 CC (RANKL) ectodomain. The three-dimensional structural representation of a  
 CC RANKL ectodomain crystal complex, is useful for identifying a RANK or  
 CC osteoprotegerin (OPG) modulating compound, and for identifying a compound  
 CC with RANK modulating activity. The crystals permit the determination of  
 CC the three-dimensional X-ray diffraction structure of the crystal-line  
 CC polypeptide to high resolution. The atomic structure coordinates and  
 CC structural information which comprises atomic structure coordinates are  
 CC useful for identifying bone-forming compounds by methods which utilise  
 CC the coordinates for solving the three-dimensional X-ray diffraction  
 CC and/or solution structures of other proteins, including mutant forms, to  
 CC high resolution. The structural information may also be used in a variety  
 CC of molecular modeling and computer-based screening applications to, for  
 CC example design mutants of the crystallized RANKL, its receptors, or a  
 CC portion or fragment of RANKL or its receptors. The coordinates of RANKL  
 CC crystal, or subsets of such structural coordinates of the RANKL crystal,  
 CC are useful for designing or identifying candidate compounds capable of  
 CC modulating RANK biological activity, and for identifying compounds which  
 CC mimic the capability of RANKL to bind RANK molecules, thereby activating  
 CC the receptor. The present sequence represents the amino acid sequence of  
 CC the tumour necrosis factor family cytokine, TRAIL.

XX Sequence 161 AA;

Query Match 66.0%; Score 850; DB 7; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-75;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSHSFSLNHLRNGELVIHEKG 142  
 Db 1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSHSFSLNHLRNGELVIHEKG 60  
 QY 143 FYYIYSQTYFRQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 202  
 Db 61 FYYIYSQTYFRQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 120  
 QY 203 SIYOGGIFELKENDRIFSVTVNEHLMDHDEASFPFAPLVG 243  
 Db 121 SIYOGGIFELKENDRIFSVTVNEHLMDHDEASFPFAPLVG 161  
 RESULT 12  
 AAU99301  
 ID AAU99301 standard; protein; 212 AA.  
 XX  
 AC AAU99301;  
 XX  
 DT 24-SEP-2002 (first entry)  
 XX  
 DE Human TRAIL splice variant 8, rpl-6-6, protein.  
 XX  
 KW Human; cytostatic; neuroprotective; immunosuppressive; splice variant;  
 KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;  
 KW TRAIL; apoptosis; programmed cell death; differentiation; development;  
 KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;  
 KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;  
 KW therapeutic; neurodegenerative disease; autoimmune disease; aging;  
 KW chromosome 3q26; rpl-6-6.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..16 /note= "Cytoplasmic domain"  
 FT Domain 17..38 /note= "Transmembrane domain"  
 FT Domain 39..212 /note= "Extracellular domain"  
 FT Misc-difference 209 /note= "Encoded by in-frame stop codon"  
 FT  
 XX US2002061525-A1.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 16-MAY-2001; 2001US-00855544.  
 XX  
 PR 16-MAY-2000; 2000IL-00136156.  
 XX  
 PA (VELI/) YELIN R.  
 PA (KHOS/) KHOSRAVI R.  
 PA (SAVI/) SAVITZKY K.  
 XX  
 PI Yelin R, Khosravi R, Savitzky K;  
 XX  
 DR WPI; 2002-479259/51.  
 XX  
 PT New splice variants of tumor necrosis factor-related apoptosis inducing  
 PT ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat  
 PT diseases or disorders associated with low expression of the variants.  
 XX  
 PS Claim 4; Fig 8; 29pp; English.  
 XX  
 CC The invention discloses isolated, naturally occurring, polypeptide splice  
 CC variants of human tumour necrosis factor (TNF)-related apoptosis inducing  
 CC ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal  
 CC cellular differentiation and development of multicellular organisms.  
 CC Apoptosis is induced by certain cytokines which include TNF and TRAIL  
 CC (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane  
 CC protein which induces apoptosis and nuclear factor-B (NF-B) activation in  
 CC many tissues and cells. Receptors for TRAIL include two death domain

CC containing receptors, DR4 and DR5, as well as two decoy receptors, Dcrl  
 CC and Dcrl2, lacking the intracellular signalling death domain. TRAIL,  
 CC induced by type I interferons, induces apoptosis in tumour cells, whereas  
 CC normal cells are relatively resistant without showing significant toxic  
 CC side effects. Thus, TRAIL has the potential to be a very useful  
 CC antitumour agent. The naturally occurring splice variants may differ in  
 CC their cellular distribution, expression levels/timing and activity.  
 CC Determining these factors could provide possible mechanisms for the  
 CC induction of apoptosis of tumour cells. The splice variant polypeptides  
 CC and polynucleotides can be used in gene therapy, to raise antibodies, to  
 CC detect the levels, distribution and ratios of expression of TRAIL, and  
 CC its splice variants, in a biological sample and to identify compounds  
 CC which bind the variant TRAIL products and modulate its activity (agonists  
 CC and antagonists). Pharmaceutical compositions, comprising an expression  
 CC vector or any of the amino acid sequences, are useful for causing a  
 CC cytotoxic effect in cancer cells and for treatment of diseases which can  
 CC be ameliorated, cured or prevented by lowering or raising the level of  
 CC the amino acid sequences. The antibodies may also have a therapeutic  
 CC utility in blocking or decreasing the activity of the TRAIL variant  
 CC products. Diseases that may be treated include cancer, neurodegenerative  
 CC diseases, autoimmune diseases, diseases involved in the non-normal  
 CC development of tissues and aging. TRAIL's gene is located on chromosome  
 CC 3q26. The sequence presented is the human TNF-related apoptosis inducing  
 CC ligand (TRAIL) splice variant 8, rpl-6-6, protein which has had an C-  
 CC terminal section of the conserved TNF domain deleted  
 XX  
 SQ Sequence 212 AA;  
 Query Match 64.3%; Score 827; DB 5; Length 212;  
 Best Local Similarity 91.3%; Pred. No. 2.4e-72;  
 Matches 158; Conservative 5; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMSPGQVQWQLRQLVKMLRTSEE 60  
 Db 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMSPGQVQWQLRQLVKMLRTSEE 98  
 QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120  
 Db 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158  
 QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRQBEIKENTKNDKQVQYIY 173  
 Db 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRQBEIKENTKNDKQVQYIY 211  
 RESULT 13  
 ADI53053  
 ID ADI53053 standard; protein; 154 AA.  
 XX  
 AC ADI53053;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Human TRAIL protein (aa 119-281).  
 XX  
 KW protein co-ordinate data; cytostatic; antiallergic; immunosuppressive;  
 KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;  
 KW antidiabetic; dermatological; antiasthmatic; neutrokin-alpha;  
 KW crystallography; cancer; allergic disorder; autoimmune disease;  
 KW rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes;  
 KW systemic lupus erythematosus; asthma.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..154 /note= "X shown in the sequence are illegible in the  
 FT figure sequence"  
 FT  
 XX WO2003050134-A2.  
 XX  
 PD 19-JUN-2003.  
 XX

PF 07-NOV-2002; 2002WO-US035661.  
XX  
PR 07-NOV-2001; 2001US-0331049P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Li Y, Oren DE, Arnold E, Volovik Y;  
FI WPI; 2003-532895/50.  
XX  
XX  
XX New crystalline Neutrokinine-alpha protein, useful for designing compounds  
PT that bind, inhibit or mimic a Neutrokinine-alpha protein or enhance the  
PT activity of a Neutrokinine-alpha protein for treating e.g. cancer or  
PT allergic disorders.  
XX  
XX  
XX Disclosure; Fig 1; 362pp; English.  
PS  
XX The invention relates to a neutrokinine-alpha protein in crystalline form.  
CC The crystalline neutrokinine-alpha protein is useful for designing  
CC molecules that have biological activity or compounds that bind, inhibit  
CC or mimic a neutrokinine-alpha protein and/or enhance the activity of a  
CC neutrokinine-alpha protein. The three-dimensional structure of a neutrokinine  
CC -alpha protein is useful in determining the three-dimensional of other  
CC neutrokinine-alpha proteins and their homologs. The compounds that mimic,  
CC prevent or inhibit the activity of the protein are useful for treating  
CC cancer, allergic disorders, or autoimmune diseases such as rheumatoid  
CC arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus  
CC erythematosus or asthma. This sequence represents the human TRAIL protein  
CC amino acids 119-281 which is used in the invention for comparison to the  
CC human neutrokinine-alpha protein (ADI53050).  
XX  
XX SQ Sequence 154 AA;  
SQ

Query Match 59.4%; Score 764.5; DB 7; Length 154;  
Best Local Similarity 90.8%; Pred. No. 2e-66;  
Matches 148; Conservative 0; Mismatches 6; Indels 9; Gaps 1;  
Qy 81 PQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIE 140  
Db 1 PQVAAHITGKRGK-----KNEKALGRKINSWESSRSGHSLNHLRNGELVIE 51  
Qy 141 KGFYIYSQTYFRQBEIKENTKDKQKQVQIYKYTSYDPDPILLMKSGNSKDAEYG 200  
Db 52 KGFYIYSQTYFRQBEIKENTKDKQKQVQIYKYTSYDPDPILLMKSGNSKDAEYG 111  
Qy 201 LYSIQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 243  
Db 112 LYSIQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 154

RESULT 14  
ADO24774  
ID ADO24774 standard; protein; 171 AA.  
XX  
AC ADO24774;  
XX  
XX 29-JUL-2004 (first entry)  
DT  
XX  
DE Cat soluble TRAIL protein.  
XX  
XX cytosolic; dermatological; antirheumatic; antiarthritic;  
KW neuroprotective; canine; feline; TNF-related apoptosis-inducing ligand;  
KW TRAIL; apoptosis; cancer; neurodegenerative disease; lupus erythematosus;  
KW rheumatoid arthritis; multiple sclerosis; diagnosis; genetic testing;  
KW angiogenesis.  
XX  
XX Felis catus.  
XX  
XX WO2004039307-A2.  
XX  
XX 13-MAY-2004.  
XX  
XX 21-OCT-2003; 2003WO-IB004635.  
XX  
XX 21-OCT-2003; 2003WO-IB004635.

XX 30-OCT-2002; 2002US-0422342P.  
XX (PFIZ ) PFIZER PROD INC.  
XX  
XX Cai JH, Rong S;  
XX  
XX WPI; 2004-376043/35.  
XX N-PSDB; ADO24773.  
XX  
XX Novel isolated canine or feline TNF-related apoptosis-inducing ligand  
PT polypeptide, useful for diagnostic evaluation, genetic testing and/or  
PT prognosis of angiogenesis-related disorders, such as cancer.  
XX  
XX Disclosure; SEQ ID NO 29; 151pp; English.  
XX  
XX The invention relates to an isolated polypeptide (I) comprising a canine  
CC or feline TNF-related apoptosis-inducing ligand (TRAIL) sequence and  
CC optionally a fusion peptide fused to the polypeptide. Modulators of (I)  
CC are useful for treating an apoptosis-related disorder in a subject. The  
CC apoptosis-related disorder is chosen from cancer, neurodegenerative  
CC disease, lupus erythematosus, rheumatoid arthritis and multiple  
CC sclerosis. (I) is useful for diagnostic evaluation, genetic testing  
CC and/or prognosis of angiogenesis-related disorders, such as cancer. This  
CC sequence represents a gene encoding a cat soluble TRAIL protein used in  
CC the invention.  
XX  
XX SQ Sequence 171 AA;  
SQ

Query Match 59.4%; Score 764; DB 8; Length 171;  
Best Local Similarity 84.2%; Pred. No. 2.6e-66;  
Matches 144; Conservative 13; Mismatches 12; Indels 2; Gaps 1;  
Qy 75 LVREGRQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNG 134  
Db 1 MVREGRQVAAHITGTRRRSTFPVPSSKNEKALGOKINSWESSRKGHSLNHLRNG 60  
Qy 135 ELVIEHKGFTYIYSQTYFRFQ--BEIKENTKDKQKQVQIYKYTSYDPDPILLMKSGNSC 192  
Db 61 ELVHQRGFTYIYSQTYFRFQBEETEONRKNKQKQVQIYKYTSYDPDPILLMKSGNSC 120  
Qy 193 WSKDAEYGLYSIQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 243  
Db 121 WSKDSEYGLYSIQGGIFELKENDRIFSVTNEHLIDMDQEQEASFFGAFVLG 171

RESULT 15  
ADO24776  
ID ADO24776 standard; protein; 201 AA.  
XX  
AC ADO24776;  
XX  
XX 29-JUL-2004 (first entry)  
DT  
XX  
DE Cat soluble TRAIL with a C-terminal V5-His tag protein.  
XX  
XX cytosolic; dermatological; antirheumatic; antiarthritic;  
KW neuroprotective; canine; feline; TNF-related apoptosis-inducing ligand;  
KW TRAIL; apoptosis; cancer; neurodegenerative disease; lupus erythematosus;  
KW rheumatoid arthritis; multiple sclerosis; diagnosis; genetic testing;  
KW angiogenesis.  
XX  
XX Felis catus.  
XX  
XX WO2004039307-A2.  
XX  
XX 13-MAY-2004.  
XX  
XX 21-OCT-2003; 2003WO-IB004635.  
XX  
XX 30-OCT-2002; 2002US-0422342P.  
XX  
XX (PFIZ ) PFIZER PROD INC.

```

XX
PI Cai JH, Rong S;
XX
DR WPI; 2004-376043/35.
DR N-PSDB; ADO24775.
XX
PT Novel isolated canine or feline TNF-related apoptosis-inducing ligand
PT polypeptide, useful for diagnostic evaluation, genetic testing and/or
PT prognosis of angiogenesis-related disorders, such as cancer.
XX
XX Disclosure; SEQ ID NO 31; 151pp; English.
XX
XX The invention relates to an isolated polypeptide (I) comprising a canine
CC or feline TNF-related apoptosis-inducing ligand (TRAIL) sequence and
CC optionally a fusion peptide fused to the polypeptide. Modulators of (I)
CC are useful for treating an apoptosis-related disorder in a subject. The
CC apoptosis-related disorder is chosen from cancer, neurodegenerative
CC disease, lupus erythematosus, rheumatoid arthritis and multiple
CC sclerosis. (I) is useful for diagnostic evaluation, genetic testing
CC and/or prognosis of angiogenesis-related disorders, such as cancer. This
CC sequence represents a gene encoding a cat TRAIL protein with a V5-His Tag
CC at the C-terminus and used in the invention.
XX
SQ Sequence 201 AA;
Query Match 59.4%; Score 764; DB 8; Length 201;
Best Local Similarity 84.2%; Pred. No. 3.3e-66;
Matches 144; Conservative 13; Mismatches 12; Indels 2; Gaps 1;
QY 75 LVREGRGQVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNG 134
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MVRERGFQVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNG 60
QY 135 ELVIHERGFYIYSQTYFRQ--EEIKENTKNDKQVQYIYKTSYDPDILLMKSARNSC 192
Db ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 ELVIHORGFYIYSQTYFRQPEETEQRNKRKQVQYIYKTSYDPDILLMKSARNSC 120
QY 193 WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPLVG 243
Db ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 WSKDSEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAPLVG 171

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Search completed: June 3, 2005, 06:40:57  
Job time : 164 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2005, 06:44:02 ; Search time 139 Seconds  
(without alignments)  
604.318 Million cell updates/sec

Title: US-10-662-431-2\_COPY\_39\_281

Perfect score: 1287

Sequence: 1 TNELKQMDKXKSGIACPL.....NEHLIDMDHEASFGAPLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 944584

Minimum DB seq length: 0

Maximum DB seq length: 243

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubaa/PCT\_NEW\_PUB.pep.\*  
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17: /cgn2\_6/ptodata/1/pubaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	892.5	69.3	228	17	US-10-855-559-4
2	887	68.9	168	9	US-09-900-530A-10
3	887	68.9	168	17	US-10-981-989-14
4	878	68.2	166	9	US-09-779-050A-16
5	859	66.7	164	13	US-10-116-378-29
6	859	66.7	164	17	US-10-959-537-29
7	850	66.0	161	14	US-10-216-074-7
8	849	66.0	161	14	US-10-338-083-11
9	849	66.0	161	16	US-10-611-399-11
10	849	66.0	161	17	US-10-794-751-11
11	835	64.9	158	17	US-10-778-890-10
12	826	64.2	208	9	US-09-855-544A-16
13	746.5	58.0	188	9	US-09-855-544A-14

14	636	49.4	172	9	US-09-779-050A-17
15	446	34.7	85	14	US-10-286-696-12
16	370	28.7	113	9	US-09-855-544A-15
17	291	22.6	98	9	US-09-855-544A-10
18	291	22.6	98	16	US-10-367-094-20
19	291	22.6	101	15	US-10-652-244-4
20	278	21.6	56	15	US-10-399-018-20
21	277	21.5	88	9	US-09-855-544A-9
22	245.5	19.1	87	14	US-10-286-696-13
23	236	18.3	178	15	US-10-338-785A-2
24	236	18.3	178	16	US-10-611-363-2
25	233.5	18.1	199	14	US-10-050-902-224
26	233.5	18.1	199	14	US-10-050-898-224
27	233.5	18.1	199	15	US-10-289-456-86
28	232.5	18.1	151	14	US-10-338-083-10
29	232.5	18.1	151	16	US-10-611-399-10
30	232.5	18.1	151	17	US-10-794-751-10
31	232.5	18.1	158	15	US-10-289-456-101
32	232.5	18.1	159	11	US-09-933-915A-8
33	232.5	18.1	159	15	US-10-289-456-84
34	232.5	18.1	160	9	US-09-779-050A-15
35	232.5	18.1	160	11	US-09-933-915A-7
36	232.5	18.1	165	15	US-10-289-456-103
37	232.5	18.1	173	11	US-09-933-915A-6
38	232.5	18.1	178	11	US-09-933-915A-5
39	232.5	18.1	178	15	US-10-289-456-83
40	232.5	18.1	180	15	US-10-289-456-100
41	232.5	18.1	181	11	US-09-933-915A-4
42	232.5	18.1	185	14	US-10-050-902-320
43	232.5	18.1	185	14	US-10-050-898-320
44	232.5	18.1	186	16	US-10-467-243-16
45	232.5	18.1	187	15	US-10-289-456-102

#### ALIGNMENTS

#### RESULT 1

US-10-855-559-4  
; Sequence 4, Application US/10855559  
; Publication No. US20050031593A1  
; GENERAL INFORMATION:  
; APPLICANT: Harding, Thomas  
; APPLICANT: Jooss, Karin  
; APPLICANT: Lalani, Alshad  
; APPLICANT: Donahue, Brian  
; TITLE OF INVENTION: Method for Treating Cancer By Vector-Mediated Delivery of  
; FILE REFERENCE: 3802-094-27  
; CURRENT APPLICATION NUMBER: US/10/855,559  
; CURRENT FILING DATE: 2004-05-28  
; PRIOR APPLICATION NUMBER: US 60/475,006  
; FILING DATE: 2003-06-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-855-559-4

Query Match 69.3%; Score 892.5; DB 17; Length 228;  
Best Local Similarity 85.7%; Pred. No. 2.3e-74;  
Matches 174; Conservative 5; Mismatches 13; Indels 11; Gaps 1;  
Qy 52 KMLTSTSEETISTVQEKQNISPL-----VREERGQVAAHTTGRGRSNTLSS 100  
Db 26 KQIEDKTEELISKYIHIENEIARIKKUIGREGRGVRGQVAAHTTGRGRSNTLSS 85  
Qy 101 PMSKNEKALGRKINSWESSRSGHSFLSNLHNLNRELVIHEKGFYIYSQTYFRQEEIKE 160  
Db 86 PMSKNEKALGRKINSWESSRSGHSFLSNLHNLNRELVIHEKGFYIYSQTYFRQEEIKE 145

Qy 161 NTKNDKQWQYIYKTSYPPDPILLMKSAKNSWCKDAEYGLYSIQGGIFELKENDRIFV 220  
Db 146 NTKNDKQWQYIYKTSYPPDPILLMKSAKNSWCKDAEYGLYSIQGGIFELKENDRIFV 205  
Qy 221 SVTNEHLIDMDHEASFFGAFVLG 243  
Db 206 SVTNEHLIDMDHEASFFGAFVLG 228

## RESULT 2

US-09-900-530A-10  
; Sequence 10, Application US/09900530A  
; Patent No. US20020128438A1  
; GENERAL INFORMATION:  
; APPLICANT: Seol, Dae-Wu  
; APPLICANT: Billiar, Timothy R.  
; TITLE OF INVENTION: DNA Cassette for the Production of  
; TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline  
; TITLE OF INVENTION: /Doxycycline-Inducible Adeno-Associated Virus Vector, Their  
; TITLE OF INVENTION: Combination and Use in Gene Therapy  
; FILE REFERENCE: 5006-1-002  
; CURRENT APPLICATION NUMBER: US/09/900,530A  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: KR 2000-38441  
; PRIOR FILING DATE: 2000-07-06  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-900-530A-10

Query Match 68.9%; Score 887; DB 9; Length 168;  
Best Local Similarity 100.0%; Pred. No. 5.1e-74;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 VREGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 135  
Db 1 VREGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 60  
Qy 136 LVIHEKGFYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYPPDPILLMKSAKNSWCK 195  
Db 61 LVIHEKGFYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYPPDPILLMKSAKNSWCK 120  
Qy 196 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243  
Db 121 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 168

## RESULT 3

US-10-981-989-14  
; Sequence 14, Application US/10981989  
; Publication No. US2005013328A1  
; GENERAL INFORMATION:  
; APPLICANT: Devi, Gayathri  
; APPLICANT: Iversen, Patrick L.  
; TITLE OF INVENTION: Method and Antisense Compound for Potentiating Anti-Cancer Agents  
; FILE REFERENCE: 50450.8058.US00  
; CURRENT APPLICATION NUMBER: US/10/981,989  
; CURRENT FILING DATE: 2004-11-04  
; PRIOR APPLICATION NUMBER: 60/518,139  
; PRIOR FILING DATE: 2003-11-06  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 14  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-981-989-14

Query Match 68.9%; Score 887; DB 17; Length 168;  
Best Local Similarity 100.0%; Pred. No. 5.1e-74;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 76 VREGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 135  
Db 1 VREGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 60  
Qy 136 LVIHEKGFYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYPPDPILLMKSAKNSWCK 195  
Db 61 LVIHEKGFYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYPPDPILLMKSAKNSWCK 120  
Qy 196 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243  
Db 121 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 168

## RESULT 4

US-09-779-050A-16  
; Sequence 16, Application US/09779050A  
; Patent No. US20020160416A1  
; GENERAL INFORMATION:  
; APPLICANT: BOYLE, WILLIAM  
; APPLICANT: HSU, HAILING  
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY  
; FILE REFERENCE: A-570B  
; CURRENT APPLICATION NUMBER: US/09/779,050A  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 60/181,800  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-050A-16

Query Match 68.2%; Score 878; DB 9; Length 166;  
Best Local Similarity 100.0%; Pred. No. 3.4e-73;  
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 ERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 137  
Db 1 ERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 60  
Qy 138 IHEKGFYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYPPDPILLMKSAKNSWCKDA 197  
Db 61 IHEKGFYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYPPDPILLMKSAKNSWCKDA 120  
Qy 198 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243  
Db 121 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 166

## RESULT 5

US-10-116-378-29  
; Sequence 29, Application US/10116378  
; Publication No. US20020150993A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin  
; APPLICANT: Marsters, Scot A.  
; APPLICANT: Pitti, Robert M.  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND  
; TITLE OF INVENTION: NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P1206R1  
; CURRENT APPLICATION NUMBER: US/10/116,378  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087

;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09  
;; NUMBER OF SEQ ID NOS: 31  
;; SEQ ID NO 29  
;; LENGTH: 164  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-116-378-29

Query Match 66.7%; Score 859; DB 13; Length 164;  
Best Local Similarity 99.4%; Pred. No. 1.9e-71;  
Matches 163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 80 GPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIH 139  
Db 1 GPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIH 60  
  
Qy 140 EKGFFYYISQTYFRFQEEIKENTKNDKQVQYIYKTSYTPDPILLMKSRNSCWSDAEY 199  
Db 61 EKGFFYYISQTYFRFQEEIKENTKNDKQVQYIYKTSYTPDPILLMKSRNSCWSDAEY 120  
  
Qy 200 GLYSIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 243  
Db 121 GLYSIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 164

RESULT 6  
US-10-959-537-29  
;; Sequence 29, Application US/10959537  
;; Publication No. US20050069983A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Gurney, Austin  
;; APPLICANT: Marsters, Scot A.  
;; APPLICANT: Pitti, Robert M.  
;; APPLICANT: Wood, William  
;; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC  
;; FILE REFERENCE: P1206R1  
;; CURRENT APPLICATION NUMBER: US/10/959,537  
;; PRIOR FILING DATE: 2004-10-06  
;; PRIOR APPLICATION NUMBER: US/09/247,225  
;; PRIOR FILING DATE: 1999-02-09  
;; PRIOR APPLICATION NUMBER: US 60/074,087  
;; PRIOR FILING DATE: 1998-02-09  
;; NUMBER OF SEQ ID NOS: 31  
;; SEQ ID NO 29  
;; LENGTH: 164  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-959-537-29

Query Match 66.7%; Score 859; DB 17; Length 164;  
Best Local Similarity 99.4%; Pred. No. 1.9e-71;  
Matches 163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 80 GPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIH 139  
Db 1 GPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIH 60  
  
Qy 140 EKGFFYYISQTYFRFQEEIKENTKNDKQVQYIYKTSYTPDPILLMKSRNSCWSDAEY 199  
Db 61 EKGFFYYISQTYFRFQEEIKENTKNDKQVQYIYKTSYTPDPILLMKSRNSCWSDAEY 120  
  
Qy 200 GLYSIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 243  
Db 121 GLYSIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 164

RESULT 7  
US-10-216-074-7  
;; Sequence 7, Application US/10216074  
;; Publication No. US2003014845A1

;; GENERAL INFORMATION:  
;; APPLICANT: Shu, Hong-Bing  
;; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND  
;; FILE REFERENCE: 2879-72  
;; CURRENT APPLICATION NUMBER: US/10/216,074  
;; CURRENT FILING DATE: 2003-03-12  
;; PRIOR APPLICATION NUMBER: US/09/565,423  
;; PRIOR FILING DATE: 2000-05-05  
;; PRIOR APPLICATION NUMBER: UNKNOWN  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: 60/132,892  
;; PRIOR FILING DATE: 1999-05-06  
;; NUMBER OF SEQ ID NOS: 17  
;; SOFTWARE: Patent in Ver. 2.1  
;; SEQ ID NO 7  
;; LENGTH: 161  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-216-074-7

Query Match 66.0%; Score 850; DB 14; Length 161;  
Best Local Similarity 100.0%; Pred. No. 1.3e-70;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 83 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 142  
Db 1 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 60  
  
Qy 143 FYIYISQTYFRFQEEIKENTKNDKQVQYIYKTSYTPDPILLMKSRNSCWSDAEYGLY 202  
Db 61 FYIYISQTYFRFQEEIKENTKNDKQVQYIYKTSYTPDPILLMKSRNSCWSDAEYGLY 120  
  
Qy 203 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 243  
Db 121 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 161

RESULT 8  
US-10-338-083-11  
;; Sequence 11, Application US/10338083  
;; Publication No. US20030166559A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Desjarlais, John R.  
;; APPLICANT: Tansey, Malu Lourdes G.  
;; APPLICANT: Dahiyat, Bassil I.  
;; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof  
;; FILE REFERENCE: A-71273-2  
;; CURRENT APPLICATION NUMBER: US/10/338,083  
;; CURRENT FILING DATE: 2003-01-16  
;; PRIOR APPLICATION NUMBER: US 60/345,805  
;; PRIOR FILING DATE: 2002-01-04  
;; PRIOR APPLICATION NUMBER: US 60/373,453  
;; PRIOR FILING DATE: 2002-04-17  
;; NUMBER OF SEQ ID NOS: 23  
;; SOFTWARE: Patent in version 3.2  
;; SEQ ID NO 11  
;; LENGTH: 161  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-338-083-11

Query Match 66.0%; Score 849; DB 14; Length 161;  
Best Local Similarity 100.0%; Pred. No. 1.6e-70;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 82 QVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEK 141  
Db 1 QVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEK 60  
  
Qy 142 GFYIYISQTYFRFQEEIKENTKNDKQVQYIYKTSYTPDPILLMKSRNSCWSDAEYGL 201  
Db 61 GFYIYISQTYFRFQEEIKENTKNDKQVQYIYKTSYTPDPILLMKSRNSCWSDAEYGL 120

QY 202 YSIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 242  
Db 121 YSIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 161

RESULT 9  
US-10-611-399-11  
; Sequence 11, Application US/10611399  
; Publication No. US20040170602A1  
; GENERAL INFORMATION:  
; APPLICANT: Desjarlais, John R.  
; APPLICANT: Tansey, Malu Lourdes G.  
; APPLICANT: Dahiyat, Bassil I.  
; TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF  
; FILE REFERENCE: A-71273-3  
; CURRENT APPLICATION NUMBER: US/10/611,399  
; CURRENT FILING DATE: 2003-07-01  
; PRIOR APPLICATION NUMBER: US 10/338,083  
; PRIOR FILING DATE: 2003-01-06  
; PRIOR APPLICATION NUMBER: US 60/345,805  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: US 60/373,453  
; PRIOR FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF

Query Match 66.0%; Score 849; DB 16; Length 161;  
Best Local Similarity 100.0%; Pred. No. 1.6e-70;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 82 QRVAAHTGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHK 141  
Db 1 QRVAAHTGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHK 60  
QY 142 GFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSNCSWCKDAEYGL 201  
Db 61 GFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSNCSWCKDAEYGL 120  
QY 202 YSIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 242  
Db 121 YSIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 161

RESULT 10  
US-10-794-751-11  
; Sequence 11, Application US/10794751  
; Publication No. US20050048626A1  
; GENERAL INFORMATION:  
; APPLICANT: Desjarlais, John R.  
; APPLICANT: Thomason, Adam Read  
; APPLICANT: Zhukovsky, Eugene Alexander  
; TITLE OF INVENTION: RAFF VARIANTS AND METHODS THEREOF  
; FILE REFERENCE: A-72175-1  
; CURRENT APPLICATION NUMBER: US/10/794,751  
; CURRENT FILING DATE: 2004-03-05  
; PRIOR APPLICATION NUMBER: US 10/338,083  
; PRIOR FILING DATE: 2003-01-06  
; PRIOR APPLICATION NUMBER: US 60/452,707  
; PRIOR FILING DATE: 2003-03-07  
; PRIOR APPLICATION NUMBER: US 60/482,081  
; PRIOR FILING DATE: 2003-06-23  
; PRIOR APPLICATION NUMBER: US 60/523,880  
; PRIOR FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: US 60/528,104  
; PRIOR FILING DATE: 2003-12-08  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 11  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-794-751-11

Query Match 66.0%; Score 849; DB 17; Length 161;  
Best Local Similarity 100.0%; Pred. No. 1.6e-70;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 82 QRVAAHTGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHK 141  
Db 1 QRVAAHTGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHK 60  
QY 142 GFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSNCSWCKDAEYGL 201  
Db 61 GFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSNCSWCKDAEYGL 120  
QY 202 YSIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 242  
Db 121 YSIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 161

RESULT 11  
US-10-778-890-10  
; Sequence 10, Application US/10778890  
; Publication No. US20050112596A1  
; GENERAL INFORMATION:  
; APPLICANT: TSCHOPP, JURG  
; TITLE OF INVENTION: APRIL-A NOVEL PROTEIN WITH GROWTH EFFECTS  
; FILE REFERENCE: A049 US  
; CURRENT APPLICATION NUMBER: US/10/778,890  
; CURRENT FILING DATE: 2004-02-12  
; PRIOR APPLICATION NUMBER: US/09/520,489  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: PCT/US98/19191  
; PRIOR FILING DATE: 1998-09-11  
; PRIOR APPLICATION NUMBER: 60/079,384  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/058,786  
; PRIOR FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-778-890-10

Query Match 64.9%; Score 835; DB 17; Length 158;  
Best Local Similarity 100.0%; Pred. No. 3.1e-69;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 85 AAHTGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHKGY 144  
Db 1 AAHTGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHKGY 60  
QY 145 YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSNCSWCKDAEYGLYSI 204  
Db 61 YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSNCSWCKDAEYGLYSI 120  
QY 205 YQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 242  
Db 121 YQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 158

RESULT 12  
US-09-855-544A-16  
; Sequence 16, Application US/09855544A  
; Patent No. US20020061525A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodrigo YELIN et al.  
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS



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; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855.544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-855-544A-16

Query Match          64.2%; Score 826; DB 9; Length 208;
Best Local Similarity 96.3%; Pred. No. 3e-68;
Matches 156; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQRLQRLVRKMLRTSEE 60
    |||||
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQRLQRLVRKMLRTSEE 98
    |||||

QY 61 TISTVQEKQNIISPLVRERGQRVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120
    |||||
Db 99 TISTVQEKQNIISPLVRERGQRVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158
    |||||

QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFOBEIKENT 162
    |||||
Db 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFOBKCKKTS 200
    |||||

RESULT 13
US-09-855-544A-14
; Sequence 14, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855.544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-855-544A-14

Query Match          58.0%; Score 746.5; DB 9; Length 188;
Best Local Similarity 61.7%; Pred. No. 6.1e-61;
Matches 150; Conservative 0; Mismatches 0; Indels 93; Gaps 1;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQRLQRLVRKMLRTSEE 60
    |||||
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQRLQRLVRKMLRTSEE 98
    |||||

QY 61 TISTVQEKQNIISPLVRERGQRVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120
    |||||
Db 99 TISTVQ----- 104
    |||||

QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFOBEIKENTKDKQKQVYIYKTSYPD 180
    |||||
Db 105 -----ENTKDKQKQVYIYKTSYPD 125
    |||||

QY 181 PILLMSARNCSWKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
    |||||
Db 126 PILLMSARNCSWKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 185
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QY 241 LVG 243
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Db 186 LVG 188
    |||

RESULT 14
US-09-779-050A-17

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; Sequence 17, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSH, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-779-050A-17

Query Match          49.4%; Score 636; DB 9; Length 172;
Best Local Similarity 71.4%; Pred. No. 9.3e-51;
Matches 120; Conservative 20; Mismatches 22; Indels 6; Gaps 1

QY 81 PQVAAHITGTRGSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVTHE 140
Db 4 PQVAAHITGTRRSNALIPISKDGKTLGOKIESWESSRRKGSFSLNHLVFRNGELVTEQ 63

QY 141 KGFYIYSQTYFRFQBE-----IKENTKNDKQMVQVIYKYTSYDPDPILLMKSARNCSWS 194
Db 64 EGLYIYSQTYFRFQEAEDAKWVKDKVTKQLVQVIYKYTSYDPDPVLMKSARNCSWS 123

QY 195 KDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIV 242
Db 124 RDAEYGLYSIQGGLFELKNDKDRIFVSVTNEHLMDLDOEASFAGAFII 171

RESULT 15
US-10-286-696-12
; Sequence 12, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; TITLE OF INVENTION: Fhm, A No. US20030129706A1e1 Member of the TNF Ligand S
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-696-12

Query Match          34.7%; Score 446; DB 14; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 78 ERGPQVAAHITGTRGSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELV 137
Db 1 ERGPQVAAHITGTRGSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELV 60

QY 138 IHEKGFYIYSQTYFRFQBEIKENT 162
Db 61 IHEKGFYIYSQTYFRFQBEIKENT 85

Search completed: June 3, 2005, 06:57:06
Job time : 141 secs

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Search completed: June 3, 2005, 06:57:06  
Job time : 141 secs

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 06:38:16 ; Search time 42 Seconds  
(without alignments)  
431.898 Million cell updates/sec

Title: US-10-662-431-2\_COPY\_39\_281  
Perfect score: 1287  
Sequence: 1 TNELKQWQDKYKSGIACFL.....NEHLIDMDHEASFGAFVLG 243

Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 410927

Minimum DB seq length: 0  
Maximum DB seq length: 243

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	930	72.3	177	3	US-09-105-343A-7
2	850	66.0	161	4	US-09-565-423-7
3	654	50.8	183	3	US-09-105-343A-8
4	544	42.3	169	4	US-09-563-611C-29
5	446	34.7	85	4	US-09-632-287A-12
6	425	33.0	121	4	US-09-513-999C-7833
7	292	22.7	120	4	US-09-569-611C-32
8	291	22.6	101	1	US-08-670-354-4
9	291	22.6	101	3	US-09-320-424-4
10	291	22.6	101	4	US-09-825-563-4
11	291	22.6	101	5	PCT-US96-10895-4
12	291	22.6	122	4	US-09-569-611C-31
13	245.5	19.1	87	4	US-09-632-287A-13
14	228.5	17.8	173	4	US-09-396-937-10
15	228.5	17.8	173	4	US-09-396-937-12
16	228.5	17.8	187	4	US-09-396-937-8
17	210	16.3	182	4	US-09-396-937-16
18	208	16.2	188	4	US-09-396-937-14
19	202.5	15.7	173	4	US-09-396-937-20
20	195.5	15.2	173	4	US-09-396-937-18
21	189.5	14.7	179	3	US-08-339-214-22
22	182.5	14.2	186	4	US-09-254-180C-175
23	182	14.1	138	3	US-08-339-214-20
24	181.5	14.1	178	3	US-08-339-214-84
25	181.5	14.1	179	3	US-08-649-100-9
26	181.5	14.1	179	3	US-08-339-214-6
27	181.5	14.1	179	4	US-09-254-180C-176

28	179	13.9	137	3	US-08-339-214-18	Sequence 18, Appl
29	178	13.8	145	3	US-08-630-172-5	Sequence 5, Appl
30	178	13.8	145	3	US-09-375-419-5	Sequence 5, Appl
31	177.5	13.6	179	3	US-08-339-214-14	Sequence 14, Appl
32	175.5	13.6	149	3	US-08-584-031-17	Sequence 17, Appl
33	175.5	13.6	149	4	US-09-934-465-17	Sequence 17, Appl
34	175	13.6	148	4	US-09-582-450-17	Sequence 17, Appl
35	175	13.6	152	4	US-09-496-118B-8	Sequence 8, Appl
36	173	13.4	138	3	US-08-339-214-4	Sequence 4, Appl
37	173	13.4	138	3	US-08-339-214-12	Sequence 12, Appl
38	173	13.4	138	3	US-08-339-214-81	Sequence 81, Appl
39	173	13.4	138	4	US-09-565-423-5	Sequence 5, Appl
40	173	13.4	138	4	US-09-254-180C-177	Sequence 177, Appl
41	173	13.4	139	3	US-08-339-214-80	Sequence 80, Appl
42	173	13.4	139	4	US-08-968-686-4	Sequence 4, Appl
43	173	13.4	141	3	US-09-286-529-22	Sequence 22, Appl
44	173	13.4	141	3	US-08-339-214-79	Sequence 79, Appl
45	170	13.2	136	3	US-08-339-214-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1  
US-09-105-343A-7  
; Sequence 7, Application US/09105343A  
; Patent No. 6207642  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, S.R.  
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
; FOR TREATMENT AND DIAGNOSIS OF DISEASE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-6050  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/105,343A  
; FILING DATE: 12-FEB-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/02859  
; FILING DATE: 12-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BECKER, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6048.US.P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847-935-1729  
; TELEFAX: 847-938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6207642e  
US-09-105-343A-7

Query Match 72.3%; Score 930; DB 3; Length 177;  
Best Local Similarity 99.4%; Pred. No. 1.6e-88;  
Matches 176; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 67 EKQNISPLVREGRQVAAHITGRGNTSLSPNSKNEKALGRKINSWESSRCHSFL 126

Db 1 EKOQNISPLVRERGPQVAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 60  
Qy 127 SNLHLRNGELVIEHKGFFYIYSQTYFRQBEIKENTKNDKQMVYIYKYTSYDPILLMK 186  
Db 61 SNLHLRNGELVIEHKGFFYIYSQTYFRQBEIKENTKNDKQMVYIYKYTSYDPILLMK 120  
Qy 187 SARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 243  
Db 121 SARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 177

RESULT 2  
US-09-565-423-7  
; Sequence 7, Application US/09565423  
; Patent No. 6475987  
; GENERAL INFORMATION:  
; APPLICANT: Shu, Hong-Bing  
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 2879-72  
; CURRENT APPLICATION NUMBER: US/09/565,423  
; CURRENT FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: UNKNOWN  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/132,892  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-565-423-7

Query Match 66.0%; Score 850; DB 4; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.9e-80;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKG 142  
Db 1 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKG 60  
Qy 143 FYIYSQTYFRQBEIKENTKNDKQMVYIYKYTSYDPILLMK SARNSCWSKDAEYGLY 202  
Db 61 FYIYSQTYFRQBEIKENTKNDKQMVYIYKYTSYDPILLMK SARNSCWSKDAEYGLY 120  
Qy 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 243  
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 161

RESULT 3  
US-09-105-343A-8  
; Sequence 8, Application US/09105343A  
; Patent No. 6207642  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, S.R.  
; TITLE OF INVENTION: MEMBER OF THE TNP FAMILY USEFUL  
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-6050  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/105,343A  
; FILING DATE: 12-FEB-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/02859  
; FILING DATE: 12-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BECKER, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6048.US.P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847-935-1729  
; TELEFAX: 847-938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 183 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6207642e  
US-09-105-343A-8

Query Match 50.8%; Score 654; DB 3; Length 183;  
Best Local Similarity 68.7%; Pred. No. 7.6e-60;  
Matches 125; Conservative 22; Mismatches 29; Indels 6; Gaps 1;

Qy 67 EKOQNISPLVRERGPQVAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 126  
Db 1 EKQLSTPLPRGGRPQKVAHITGTRRSNSALIPISKDGKTLGQKTESWESSRKGHSFL 60  
Qy 127 SNLHLRNGELVIEHKGFFYIYSQTYFRQBEIKENTKNDKQMVYIYKYTSYDP 180  
Db 61 NHVLFNGELVIEQEGLYIYSQTYFRQBEIKENTKNDKQMVYIYKYTSYDP 120  
Qy 181 PILLMK SARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
Db 121 PIVLMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 180  
Qy 241 LV 242  
Db 181 II 182

RESULT 4  
US-09-569-611C-29  
; Sequence 29, Application US/09569611C  
; Patent No. 6720182  
; GENERAL INFORMATION:  
; APPLICANT: SAVITZKY et al.  
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS  
; FILE REFERENCE: 2786-0151P  
; CURRENT APPLICATION NUMBER: US/09/569,611C  
; CURRENT FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 169  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-569-611C-29

Query Match 42.3%; Score 544; DB 4; Length 169;  
Best Local Similarity 99.0%; Pred. No. 1.8e-48;  
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDQKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKWLQRLVKMLRTSEE 60  
Db 63 TNELKQMDQKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKWLQRLVKMLRTSEE 122  
Qy 61 TISTVQEKQONISPLVRERGPQVAHITGRSNTLSSPNSK 104

Db 123 TISTVQEKQONISPLVRERGQVAAHITGTRGNTLSSPNSR 166

## RESULT 5

US-09-632-287A-12  
; Sequence 12, Application US/09632287A  
; Patent No. 6521422  
; GENERAL INFORMATION:  
; APPLICANT: Hsu, Hailing  
; APPLICANT: Wooden, Scott K  
; APPLICANT: Boyle, William J  
; TITLE OF INVENTION: Fhm, A No. 6521422e1 Member of the TNF Ligand Supergene Family  
; FILE REFERENCE: 01017/35550A  
; CURRENT APPLICATION NUMBER: US/09/632,287A  
; CURRENT FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/147,294  
; PRIOR FILING DATE: 1999-08-04  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 85  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-632-287A-12

Query Match 34.7%; Score 446; DB 4; Length 85;  
Best Local Similarity 100.0%; Pred. No. 9.6e-39;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 ERGPORVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGSLV 137

Db 1 ERGPORVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGSLV 60

Qy 138 IHEKGFYIYSQTYPRFQEEIKENT 162

Db 61 IHEKGFYIYSQTYPRFQEEIKENT 85

## RESULT 6

US-09-513-999C-7833  
; Sequence 7833, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: Patent No. 6783961  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 7833  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -32...-1  
; OTHER INFORMATION: score 5.3  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: -18  
; OTHER INFORMATION: Xaa=Asn or Thr  
US-09-513-999C-7833

Query Match 33.0%; Score 425; DB 4; Length 121;  
Best Local Similarity 100.0%; Pred. No. 2.4e-36;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELQMOMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWLRLVRMLRTSEE 60  
|||||  
Db 39 TNELQMOMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWLRLVRMLRTSEE 98  
|||||  
Qy 61 TISTVQEKQONISPLVRERG 80  
|||||  
Db 99 TISTVQEKQONISPLVRERG 118  
|||||

## RESULT 7

US-09-569-611C-32  
; Sequence 32, Application US/09569611C  
; Patent No. 6720182  
; GENERAL INFORMATION:  
; APPLICANT: SAVITZKY et al.  
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS  
; FILE REFERENCE: 2786-0151P  
; CURRENT APPLICATION NUMBER: US/09/569,611C  
; CURRENT FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-569-611C-32

Query Match 22.7%; Score 292; DB 4; Length 120;  
Best Local Similarity 98.1%; Pred. No. 1.5e-22;  
Matches 52; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELQMOMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWLRLVRM 53

Db 63 TNELQMOMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWLRLVRKV 115  
|||||

## RESULT 8

US-08-670-354-4  
; Sequence 4, Application US/08670354  
; Patent No. 5763223  
; GENERAL INFORMATION:  
; APPLICANT: Steven R. Wiley and  
; APPLICANT: Raymond G. Goodwin.  
; TITLE OF INVENTION: Cytokine That Induces Apoptosis  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.5.2  
; SOFTWARE: Microsoft Word, Version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/670,354  
; FILING DATE: 25-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/496,632  
; FILING DATE: 29-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/548,368  
; FILING DATE: 01-NOV-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172

; REFERENCE/DOCKET NUMBER: 2835-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 101 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-670-354-4

Query Match 22.6%; Score 291; DB 1; Length 101;  
Best Local Similarity 100.0%; Pred. No. 1.5e-22;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRLVRK 52  
Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRLVRK 90

RESULT 9  
US-09-320-424-4  
; Sequence 4, Application US/09320424  
; Patent No. 6284236  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; APPLICANT: Goodwin, Raymond G.  
; TITLE OF INVENTION: Cytokine that Induces Apoptosis  
; FILE REFERENCE: 2835-E  
; CURRENT APPLICATION NUMBER: US/09/320,424  
; CURRENT FILING DATE: 1999-05-26  
; EARLIER FILING DATE: 1998-11-10  
; EARLIER APPLICATION NUMBER: 09/048,641  
; EARLIER FILING DATE: 1998-03-26  
; EARLIER APPLICATION NUMBER: 08/670,354  
; EARLIER FILING DATE: 1996-06-25  
; EARLIER APPLICATION NUMBER: 08/548,368  
; EARLIER FILING DATE: 1995-11-01  
; EARLIER APPLICATION NUMBER: 08/496,632  
; EARLIER FILING DATE: 1995-06-29  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: human  
; US-09-320-424-4

Query Match 22.6%; Score 291; DB 3; Length 101;  
Best Local Similarity 100.0%; Pred. No. 1.5e-22;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRLVRK 52  
Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRLVRK 90

RESULT 10  
US-09-825-563-4  
; Sequence 4, Application US/09825563  
; Patent No. 6521228  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; APPLICANT: Goodwin, Raymond G.  
; TITLE OF INVENTION: Cytokine that Induces Apoptosis  
; FILE REFERENCE: 2835-E  
; CURRENT APPLICATION NUMBER: US/09/825,563  
; CURRENT FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: 09/320,424  
; PRIOR FILING DATE: 1999-05-26

; PRIOR APPLICATION NUMBER: 09/190,046  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 09/048,641  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 08/670,354  
; PRIOR FILING DATE: 1996-06-25  
; PRIOR APPLICATION NUMBER: 08/548,368  
; PRIOR FILING DATE: 1995-11-01  
; PRIOR APPLICATION NUMBER: 08/496,632  
; PRIOR FILING DATE: 1995-06-29  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: human  
; US-09-825-563-4

Query Match 22.6%; Score 291; DB 4; Length 101;  
Best Local Similarity 100.0%; Pred. No. 1.5e-22;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRLVRK 52  
Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRLVRK 90

RESULT 11  
PCT-US96-10895-4  
; Sequence 4, Application PC/TUS9610895  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation.  
; TITLE OF INVENTION: Cytokine That Induces Apoptosis  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.5.2  
; SOFTWARE: Microsoft Word, Version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/10895  
; FILING DATE: 25-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/496,632  
; FILING DATE: 29-JUN-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/548,368  
; FILING DATE: 01-NOV-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2835-WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 101 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US96-10895-4

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Query Match      22.6%; Score 291; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSKSGIACFLKEDDSYDNDPNDDESNMSPCWQVKQLRQLVRK 52
Db 39 TNELKQMDKYSKSGIACFLKEDDSYDNDPNDDESNMSPCWQVKQLRQLVRK 90

RESULT 12
US-09-569-611C-31
; Sequence 31, Application US/09569611C
; Patent No. 6720182
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/09/569,611C
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-31

Query Match      22.6%; Score 291; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 2e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSKSGIACFLKEDDSYDNDPNDDESNMSPCWQVKQLRQLVRK 52
Db 63 TNELKQMDKYSKSGIACFLKEDDSYDNDPNDDESNMSPCWQVKQLRQLVRK 114

RESULT 13
US-09-632-287A-13
; Sequence 13, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mouse
US-09-632-287A-13

Query Match      19.1%; Score 245.5; DB 4; Length 87;
Best Local Similarity 65.8%; Pred. No. 6.4e-18;
Matches 50; Conservative 9; Mismatches 14; Indels 3; Gaps 1;

Qy 81 PQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHE 140
Db 4 PQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHE 63

Qy 141 KGFYIYSQTYFRFOE 156
Db 64 E---YIYSQTYFRFOE 76

RESULT 14
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US-09-396-937-10
; Sequence 10, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA encoding
; OTHER INFORMATION: murine OPGL, residues 158-316, fused to His tag
US-09-396-937-10

Query Match      17.8%; Score 228.5; DB 4; Length 173;
Best Local Similarity 34.2%; Pred. No. 1e-15;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

Qy 86 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKGFY 145
Db 22 AHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKISNTLSNGLRVNQDGFY 71

Qy 146 IYSTYFRFOEIKENTKNDKQVQYIKYT-SYDPDILLMKSNRNSCWSDAEYGLYSI 204
Db 72 LYANICFRHHETSGVPTDYLQLMVYVYVTKSIKIPSSHNLMKGGSTKNWGSNPFHYSI 131

Qy 205 YQGIFELKENDRIFVSVTNEHLHMDHEASFEGAFV 242
Db 132 NVGGFFKLAGEEISIQVSNPSLLDPDODATYFGAFV 169

RESULT 15
US-09-396-937-12
; Sequence 12, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion of
; OTHER INFORMATION: murine OPGL, residues 158-316 with C to S
; OTHER INFORMATION: mutation, and His tag
US-09-396-937-12

Query Match      17.8%; Score 228.5; DB 4; Length 173;
Best Local Similarity 34.2%; Pred. No. 1e-15;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

Qy 86 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHGFSLNHLRNGELVTHEKGFY 145
Db 22 AHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKISNTLSNGLRVNQDGFY 71
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OM protein - protein search, using sw model

Run on: June 3, 2005, 06:16:49 ; Search time 43 Seconds  
(without alignments)  
487.823 Million cell updates/sec

Title: US-10-662-431-2  
Perfect score: 1478  
Sequence: 1 MAMVEVGGSLGTCVLIV.....NEHLIDMDHEASFGAPLVG 281

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/iaa/6B COMB.pap.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pap.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1478	100.0	281	1	US-08-670-354-2
2	1478	100.0	281	3	US-08-584-031-1
3	1478	100.0	281	3	US-08-780-436-1
4	1478	100.0	281	3	US-08-883-086-10
5	1478	100.0	281	3	US-09-320-424-2
6	1478	100.0	281	3	US-09-333-593A-6
7	1478	100.0	281	4	US-09-157-864-11
8	1478	100.0	281	4	US-09-825-563-24
9	1478	100.0	281	4	US-09-919-039-118
10	1478	100.0	281	4	US-09-582-450-1
11	1478	100.0	281	4	US-09-934-465-1
12	1478	100.0	281	4	US-10-011-125A-4
13	1478	100.0	281	5	PCT-US96-10895-2
14	1469	99.4	279	3	US-09-072-933C-3
15	1238	83.8	271	4	US-09-569-611C-30
16	988	66.8	253	3	US-09-320-424-11
17	988	66.8	253	4	US-09-825-563-11
18	988	66.8	256	3	US-09-320-424-13
19	988	66.8	256	4	US-09-825-563-13
20	930	62.9	177	3	US-09-105-343A-7
21	930	62.9	291	1	US-08-670-354-6
22	930	62.9	291	3	US-09-320-424-6
23	930	62.9	291	4	PCT-US96-10895-6
24	930	62.9	291	5	PCT-US96-10895-6
25	850	57.5	161	4	US-09-565-423-7
26	735	49.7	169	4	US-08-569-611C-29
27	654	44.2	183	3	US-09-105-343A-8

28	611	41.3	121	4	US-09-513-999C-7833	Sequence 7833, Ap
29	483	32.7	120	4	US-09-569-611C-32	Sequence 32, Appl
30	482	32.6	101	1	US-08-670-354-4	Sequence 4, Appl
31	482	32.6	101	3	US-09-320-424-4	Sequence 4, Appl
32	482	32.6	101	4	US-09-825-563-4	Sequence 4, Appl
33	482	32.6	101	5	PCT-US96-10895-4	Sequence 4, Appl
34	482	32.6	122	4	US-09-569-611C-31	Sequence 31, Appl
35	446	30.2	85	4	US-09-632-287A-12	Sequence 12, Appl
36	258.5	17.5	294	3	US-08-936-139-11	Sequence 11, Appl
37	258.5	17.5	294	3	US-08-995-659-11	Sequence 11, Appl
38	258.5	17.5	294	3	US-09-215-649A-11	Sequence 11, Appl
39	258.5	17.5	294	4	US-09-577-780-11	Sequence 11, Appl
40	258.5	17.5	294	4	US-09-577-800-11	Sequence 11, Appl
41	258.5	17.5	294	4	US-09-466-496-11	Sequence 11, Appl
42	258.5	17.5	294	4	US-09-871-856-11	Sequence 11, Appl
43	258.5	17.5	294	4	US-09-871-291-11	Sequence 11, Appl
44	258.5	17.5	294	4	US-09-877-650-11	Sequence 11, Appl
45	258.5	17.5	294	4	US-09-865-363-11	Sequence 11, Appl

## ALIGNMENTS

RESULT 1  
US-08-670-354-2  
; Sequence 2, Application US/08670354  
; Patent No. 5763223  
; GENERAL INFORMATION:  
; APPLICANT: Steven R. Wiley and  
; APPLICANT: Raymond G. Goodwin.  
; TITLE OF INVENTION: Cytokine That Induces Apoptosis  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.5.2  
; SOFTWARE: Microsoft Word, Version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/670,354  
; FILING DATE: 25-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/496,632  
; FILING DATE: 29-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/548,368  
; FILING DATE: 01-NOV-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2835-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-670-354-2

Query Match 100.0%; Score 1478; DB 1; Length 281;

Best Local Similarity 100.0%; Pred. No. 3.5e-149;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60  
Db 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60

Qy 61 DDSYWDNDPDESMNSPCQWKQRLVRLKMLRTSEETISTVQEKQONISPLVRERGPO 120  
Db 61 DDSYWDNDPDESMNSPCQWKQRLVRLKMLRTSEETISTVQEKQONISPLVRERGPO 120

Qy 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKG 180  
Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKG 180

Qy 181 FYIYSQTYFRFOBEIKENTKNDKQVQIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
Db 181 FYIYSQTYFRFOBEIKENTKNDKQVQIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

## RESULT 2

US-08-584-031-1  
; Sequence 1, Application US/08584031A  
; Patent No. 6030945  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: APO-2 LIGAND  
; FILE REFERENCE: 11669.22US03  
; CURRENT APPLICATION NUMBER: US/08/584.031A  
; CURRENT FILING DATE: 1996-01-09  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-584-031-1

Query Match 100.0%; Score 1478; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.5e-149;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60  
Db 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60

Qy 61 DDSYWDNDPDESMNSPCQWKQRLVRLKMLRTSEETISTVQEKQONISPLVRERGPO 120  
Db 61 DDSYWDNDPDESMNSPCQWKQRLVRLKMLRTSEETISTVQEKQONISPLVRERGPO 120

Qy 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKG 180  
Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKG 180

Qy 181 FYIYSQTYFRFOBEIKENTKNDKQVQIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
Db 181 FYIYSQTYFRFOBEIKENTKNDKQVQIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

## RESULT 3

US-08-780-496-1  
; Sequence 1, Application US/08780496  
; Patent No. 6046048  
; GENERAL INFORMATION:  
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim

; TITLE OF INVENTION: APO-2 Ligand  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/780,496  
; FILING DATE: 08-Jan-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P0978P1  
; TELEPHONE: 415/225-5416  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-780-496-1

Query Match 100.0%; Score 1478; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.5e-149;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60  
Db 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60

Qy 61 DDSYWDNDPDESMNSPCQWKQRLVRLKMLRTSEETISTVQEKQONISPLVRERGPO 120  
Db 61 DDSYWDNDPDESMNSPCQWKQRLVRLKMLRTSEETISTVQEKQONISPLVRERGPO 120

Qy 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKG 180  
Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKG 180

Qy 181 FYIYSQTYFRFOBEIKENTKNDKQVQIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240  
Db 181 FYIYSQTYFRFOBEIKENTKNDKQVQIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

## RESULT 4

US-08-883-086-10  
; Sequence 10, Application US/08883086  
; Patent No. 6171787  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, STEVEN  
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
; FOR TREATMENT AND DIAGNOSIS OF DISEASE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA

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; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Foremski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
US-08-883-086-10

Query Match      100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60
Db      1  MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60

Qy      61  DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db      61  DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

Qy      121  RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db      121  RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy      181  FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db      181  FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240

Qy      241  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db      241  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 5
US-09-320-424-2
; Sequence 2, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
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; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-09-320-424-2

Query Match      100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60
Db      1  MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60

Qy      61  DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db      61  DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

Qy      121  RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db      121  RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy      181  FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db      181  FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240

Qy      241  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db      241  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 6
US-09-333-593A-6
; Sequence 6, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 281
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-333-593A-6

Query Match      100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60
Db      1  MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60
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Qy 61 DDSYWDNDDESMNSPCQWKQQLRQLVRKMLRTSETISTVQEKQONISPLVRGPG 120  
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Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Qy 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDILLMKSARNCSWSDAEYGLY 240  
Db 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDILLMKSARNCSWSDAEYGLY 240  
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 7  
US-09-157-864-11  
; Sequence 11, Application US/09157864  
; Patent No. 6440694  
; GENERAL INFORMATION:  
; APPLICANT: Bienkowski, Michael J  
; APPLICANT: Mills, Cynthia J  
; APPLICANT: Jones, David A  
; TITLE OF INVENTION: TNF-Related Death Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property  
; ADDRESSEE: Legal Services  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/157,864  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerber, Lori L.  
; REGISTRATION NUMBER: 41,113  
; REFERENCE/DOCKET NUMBER: 6111.N CN1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616/833-0974  
; TELEFAX: 616/833-8897  
; TELEX: 224401  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-157-864-11

Query Match 100.0%; Score 1478; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.5e-149;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGTCLVIFVTLVLLQSLCAVAVTVYVFTNELKQMDKYSKGIACFLKE 60  
Db 1 MAMMEVQGGPSLGTCLVIFVTLVLLQSLCAVAVTVYVFTNELKQMDKYSKGIACFLKE 60  
Qy 61 DDSYWDNDDESMNSPCQWKQQLRQLVRKMLRTSETISTVQEKQONISPLVRGPG 120  
Db 61 DDSYWDNDDESMNSPCQWKQQLRQLVRKMLRTSETISTVQEKQONISPLVRGPG 120

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Qy 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDILLMKSARNCSWSDAEYGLY 240  
Db 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDILLMKSARNCSWSDAEYGLY 240  
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 8  
US-09-825-563-2  
; Sequence 2, Application US/09825563  
; Patent No. 6521228  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; APPLICANT: Goodwin, Raymond G.  
; TITLE OF INVENTION: Cytokine that Induces Apoptosis  
; FILE REFERENCE: 2835-E  
; CURRENT APPLICATION NUMBER: US/09/825,563  
; CURRENT FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: 09/320,424  
; PRIOR FILING DATE: 1999-05-26  
; PRIOR APPLICATION NUMBER: 09/190,046  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 09/048,641  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 08/670,354  
; PRIOR FILING DATE: 1996-06-25  
; PRIOR APPLICATION NUMBER: 08/548,368  
; PRIOR FILING DATE: 1995-11-01  
; PRIOR APPLICATION NUMBER: 08/496,632  
; PRIOR FILING DATE: 1995-06-29  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: human  
US-09-825-563-2

Query Match 100.0%; Score 1478; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.5e-149;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGTCLVIFVTLVLLQSLCAVAVTVYVFTNELKQMDKYSKGIACFLKE 60  
Db 1 MAMMEVQGGPSLGTCLVIFVTLVLLQSLCAVAVTVYVFTNELKQMDKYSKGIACFLKE 60  
Qy 61 DDSYWDNDDESMNSPCQWKQQLRQLVRKMLRTSETISTVQEKQONISPLVRGPG 120  
Db 61 DDSYWDNDDESMNSPCQWKQQLRQLVRKMLRTSETISTVQEKQONISPLVRGPG 120  
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Qy 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDILLMKSARNCSWSDAEYGLY 240  
Db 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTSYDPDILLMKSARNCSWSDAEYGLY 240  
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 9  
US-09-919-039-118  
; Sequence 118, Application US/09919039

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; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 059509CD1
US-09-919-039-118

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNSPCQVKWQRLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVKWQRLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120

Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240
Db 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 11
US-09-934-465-1
; Sequence 1, Application US/099344465
; Patent No. 6746668
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669-22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60

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Db 61 DDSYWDPNDEESMNSPCQVKWQRLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120

Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240
Db 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSARNCSWKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 12
US-10-011-125A-4
; Sequence 4, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
```

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; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: F1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-011-125A-4

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Qy 181 FYIYSQTYFRQBEIKENTKNDKQVQYIYKTSYDPDILLMKSARNCSWKDAEYGLY 240
Db 181 FYIYSQTYFRQBEIKENTKNDKQVQYIYKTSYDPDILLMKSARNCSWKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
```

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RESULT 13
PCT-US96-10895-2
; Sequence 2, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10895-2

Query Match      100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Qy 181 FYIYSQTYFRQBEIKENTKNDKQVQYIYKTSYDPDILLMKSARNCSWKDAEYGLY 240
Db 181 FYIYSQTYFRQBEIKENTKNDKQVQYIYKTSYDPDILLMKSARNCSWKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14
US-09-072-993C-3
; Sequence 3, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
;
US-09-072-993C-3

Query Match      99.4%; Score 1469; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 3.1e-148;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKEDD 62
Db 1 MMEVQGGPSLGQTCVLIVITVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKEDD 60
Qy 63 SYWDPNDEESMNSPCQVKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGPOV 122
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Db 61 SYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPOV 120  
Qy 123 AAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFY 182  
Db 121 AAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFY 180  
Qy 183 YIYSQTYFRFOBEIKENTKDKQMVOYIYKYTSYDPDPILLMKSARNCSWSDAEYGLYSI 242  
Db 181 YIYSQTYFRFOBEIKENTKDKQMVOYIYKYTSYDPDPILLMKSARNCSWSDAEYGLYSI 240  
Qy 243 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
Db 241 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 279

## RESULT 15

US-09-569-611C-30  
; Sequence 30, Application US/09569611C  
; Patent No. 6720182  
; GENERAL INFORMATION:  
; APPLICANT: SAVITZKY et al.  
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS  
; FILE REFERENCE: 2786-0151P  
; CURRENT APPLICATION NUMBER: US/09/569,611C  
; CURRENT FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 271  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-569-611C-30

Query Match 83.8%; Score 1238; DB 4; Length 271;  
Best Local Similarity 85.4%; Pred. NO. 1.3e-123;  
Matches 240; Conservative 2; Mismatches 5; Indels 34; Gaps 2;  
Qy 1 MANMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60  
Db 25 MANMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 84  
Qy 61 DDSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
Db 85 DDSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 130  
Qy 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
Db 131 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 190  
Qy 181 FYIYSQTYFRFOBEIKENTKDKQMVOYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240  
Db 191 FYIYSQTYFRFOBEIKENTKDKQMVOYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 250  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
Db 251 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 271

Search completed: June 3, 2005, 06:26:29  
Job time : 45 secs

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